

SEQUENCE LISTING

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<120> MATERIALS AND METHODS RELATING TO LIPID METABOLISM

<130> 28110/35915A

<150> US 60/197,137

<151> 2000-04-14

<150> US 09/714,936

<151> 2000-11-17

<150> US 09/667,298

<151> 2000-09-22

<150> US 09/631,451

<151> 2000-08-03

<150> US 09/598,042

<151> 2000-06-20

<160> 45

<170> PatentIn version 3.0

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57

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Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser Ala Phe Ser Ala
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105

acc cag gca cgg aaa ggc ttc tgg gac tac ttc agc cag acc agc ggg Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser Gln Thr Ser Gly 25 30 35	153
gac aaa ggc agg gtg gag cag atc cat cag cag aag atg gct cgc gag Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys Met Ala Arg Glu 40 45 50	201
ccc gcg acc ctg aaa gac agc ctt gag caa gac ctc aac aat atg aac Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu Asn Asn Met Asn 55 60 65	249
aag ttc ctg gaa aag ctg agg cct ctg agt ggg agc gag gct cct cgg Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser Glu Ala Pro Arg 70 75 80	297
ctc cca cag gac cgg gtg ggc atg ctg cgg cgg cag ctg cag gag gag ttg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu Gln Glu Glu Leu 85 90 95 100	345
gag gag gtg aag gct cgc ctc cag ccc tac atg gca gag gcg cac gag Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala Glu Ala His Glu 105 110 115	393
ctg gtg ggc tgg aat ttg gag ggc ttg cgg cag caa ctg aag ccc tac Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln Leu Lys Pro Tyr 120 125 130	441
acg atg gat ctg atg gag cag gtg gcc ctg cgc gtg cag gag ctg cag Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val Glu Leu Gln 135 140 145	489
gag cag ttg cgc gtg gtg ggg gaa gac acc aag gcc cag ttg ctg ggg Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala Gln Leu Leu Gly 150 155 160	537
ggc gtg gac gag gct tgg gct ttg ctg cag gga ctg cag agc cgc gtg Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu Gln Ser Arg Val 165 170 175 180	585
gtg cac cac acc ggc cgc ttc aaa gag ctc ttc cac cca tac gcc gag Val His His Thr Gly Arg Phe Lys Glu Leu Phe His Pro Tyr Ala Glu 185 190 195	633
agc ctg gtg agc ggc atc ggg cgc cac gtg cag gag ctg cac cgc agt Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu Leu His Arg Ser 200 205 210	681
gtg gct cgg cac gcc ccc gcc agc ccc cgg cgc ctc agt cgc tgc gtg Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu Ser Arg Cys Val 215 220 225	729
cag gtg ctc tcc cgg aag ctc acg ctc aag gcc aag gcc ctg cac gca Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys Ala Leu His Ala 230 235 240	777
cgc atc cag cag aac ctg gac cag ctg cgc gaa gag ctc agc aga gcc Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu Leu Ser Arg Ala 245 250 255 260	825
ttt gca ggc act ggg act gag gaa ggg gcc ggc cgg gac ccc cag atg Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Glu Pro Asp Pro Glu Met 265 270 275	873

ctc tcc gag gag gtg cgc cag cga ctt cag gct ttc cgc cag gac acc 921
 Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe Arg Gln Asp Thr
 280 285 290

tac ctg cag ata gct gcc ttc act cgc gcc atc gac cag gag act gag 969
 Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp Gln Glu Thr Glu
 295 300 305

gag gtc cag cag cag ctg gcg cca cct cca cca gcc cac agt gcc ttc 1017
 Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Glu His Ser Ala Phe
 310 315 320

gcc cca gag ttt caa caa aca gac agt gcc aag gtt ctg agc aag ctg 1065
 Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val Leu Ser Lys Leu
 325 330 335 340

cag gcc cgt ctg gat gac ctg tgg gaa gac atc act cac agc ctt cat 1113
 Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr His Ser Leu His
 345 350 355

gac cag gcc cac agc cat ctg ggg gac ccc tgaggatcta cctgccagg 1163
 Asp Gln Gly His Ser His Leu Gly Asp Pro
 360 365

cccatccca gctcctgtgc tggggagcct tggctctgag cctctagcat ggttcagtcc 1223

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Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys
35 40 45

Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu
50 55 60

Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg Pro Leu Ser Gly Ser
65 70 75 80

Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly Met Arg Arg Gln Leu
85 90 95

Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu Gln Pro Tyr Met Ala
100 105 110

Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu Gly Leu Arg Gln Gln
115 120 125

Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln Val Ala Leu Arg Val
130 135 140

Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly Glu Asp Thr Lys Ala
145 150 155 160

Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala Leu Leu Gln Gly Leu
165 170 175

Gln Ser Arg Val Val His His Thr Gly Arg Phe Lys Glu Leu Phe His
180 185 190

Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly Arg His Val Gln Glu
195 200 205

Leu His Arg Ser Val Ala Pro His Ala Pro Ala Ser Pro Ala Arg Leu
210 215 220

Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu Thr Leu Lys Ala Lys
225 230 235 240

Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp Gln Leu Arg Glu Glu
245 250 255

Leu Ser Arg Ala Phe Ala Gly Thr Gly Thr Glu Glu Gly Ala Gly Pro
260 265 270

Asp Pro Gln Met Leu Ser Glu Glu Val Arg Gln Arg Leu Gln Ala Phe
275 280 285

Arg Gln Asp Thr Tyr Leu Gln Ile Ala Ala Phe Thr Arg Ala Ile Asp
290 295 300

Gln Glu Thr Glu Glu Val Gln Gln Gln Leu Ala Pro Pro Pro Pro Gly
305 310 315 320

His Ser Ala Phe Ala Pro Glu Phe Gln Gln Thr Asp Ser Gly Lys Val
325 330 335

Leu Ser Lys Leu Gln Ala Arg Leu Asp Asp Leu Trp Glu Asp Ile Thr
340 345 350

His Ser Leu His Asp Gln Gly His Ser His Leu Gly Asp Pro
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<222> (181)..(1146)

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tcaacattca gcagaggccc cagatcagcg tctgagccag gccacaatg accaaggagg 180

atg gga tcc tgg gtg cag ctc atc aca agc gtc ggg gtg cag caa aac 228
Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn
1 5 10 15

cat cca ggc tgg aca gtg gct gga cag ttc caa gaa aag aaa cgc ttc 276
His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
20 25 30

act gaa gaa gtc att gaa tac ttc cag aag aaa gtt agc cca gtg cat 324
Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45

ctg aaa atc ctg ctg act agc gat gaa gcc tgg aag aga ttc gtg cgt 372
Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60

gtg gct gaa ttg ccc agg gaa gaa gca gat gct ctc tat gaa gct ctg 420
Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80

aag aat ctt aca cca tat gtg gct att gag gac aaa gac atg cag caa 468
Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln

85	90	95	
aaa gaa cag cag ttt agg gag tgg ttt ttg aaa gag ttt cct caa atc Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile 100 105 110			516
aga tgg aag att cag gag tcc ata gaa agg ctt cgt gtc att gca aat Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn 115 120 125			564
gag att gaa aag gtc cac aga ggc tgc gtc atc gcc aat gtg gtg tct Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser 130 135 140			612
ggc tcc act ggc atc ctg tct gtc att ggc gtt atg ttg gca cca ttt Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe 145 150 155 160			660
aca gca ggg ctg agc ctg agc att act gca gct ggg gta ggg ctg gga Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly 165 170 175			708
ata gca tct gcc acg gct ggg atc gcc tcc agc atc gtg gag aac aca Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr 180 185 190			756
tac aca agg tca gca gaa ctc aca gcc agc agg ctg act gca acc agc Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser 195 200 205			804
act gac caa ttg gag gca tta agg gac att ctg cat gac atc aca ccc Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro 210 215 220			852
aat gtg ctt tcc ttt gca ctt gat ttt gac gaa gcc aca aaa atg att Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile 225 230 235 240			900
gcg aat gat gtc cat aca ctc agg aga tct aaa gcc act gtt gga cgc Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg 245 250 255			948
cct ttg att gct tgg cga tat gta cct ata aat gtt gtt gag aca ctg Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu 260 265 270			996
aga aca cgt ggg gcc ccc acc cgg ata gtg aga aaa gta gcc cgg aac Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn 275 280 285			1044
ctg ggc aag gcc act tca ggt gtc ctt gtt gtg ctg gat gta gtc aac Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn 290 295 300			1092
ctt gtg caa gac tca ctg gac ttg cac aag ggg gca aaa tcc gag tct Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser 305 310 315 320			1140
gct gag tcgctgaggc agtgggctca ggagctggag gagaatctca atgagctcac Ala Glu			1196
ccatatccat cagagctctaa aagcaggcta ggcccaattg ttgcgggaag tcagggaccc			1256

caaacggagg gactggctga agccatggca gaagaacgtg gattgtgaag atttcatgga 1316
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<213> Homo sapiens

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His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
20 25 30

Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80

Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln
85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
100 105 110

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn
115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser
130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe
145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr
180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser

195

200

205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro
210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
225 230 235 240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
260 265 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
290 295 300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser
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Met Ala Gly Val Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys
15 20 25

atg gtc aag caa gtg act ggg aaa atg ccc atc ctc tcc tac tgg ccc 146
Met Val Lys Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro
30 35 40

tac ggc tgt cac tgc gga cta ggt ggc aga ggc caa ccc aaa gat gcc 194
Tyr Gly Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala
45 50 55

acg gac tgg tgc tgc cag acc cat gac tgc tgc tat gac cac ctg aag 242
Thr Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys

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acc cag ggg tgc ggc atc tac aag gac tat tac aga tac aac ttt tcc				290
Thr Gln Gly Cys Gly Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser				
	80	85	90	
cag ggg aac atc cac tgc tct gac aag gga agc tgg tgt gag cag cag				338
Gln Gly Asn Ile His Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln				
	95	100	105	
ctg tgt gcc tgt gac aag gag gtg gcc ttc tgc ctg aag cgc aac ctg				386
Leu Cys Ala Cys Asp Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu				
	110	115	120	
gac acc tac cag aag cga ctg cgt ttc tac tgg cgg ccc cac tgc cgg				434
Asp Thr Tyr Gln Lys Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg				
	125	130	135	
ggg cag acc cct ggg tgc tagaagccca caccctctac cctgttcctc				482
Gly Gln Thr Pro Gly Cys				
	140	145		
agcatggagc tctggcatcc ccacctcagt atctaacctg aaccagcctg gcttttcaaa				542
cactccgggg ggaggtgagt ccagcctccc ccggaacct ctaccaatgc cttctgacct				602
tctgaagctt tccgaatcct ccaggttagg gcagtagctg tgtcctctga ggggtggatgg				662
gaatcttggg agaagcccaa gcaagggagc cctcagaggt ggtgtttgga ccaaaagcatc				722
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Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys
 35 40 45

Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys
 50 55 60

Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Gly
 65 70 75 80

Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His
 85 90 95

Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp
 100 105 110

Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys
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Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg Gly Gln Thr Pro Gly
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Cys
 145

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gctgggtgaa	cagtgggtg	atg	gcg	tcc	ctg	172
	Met	Ala	Ser	Leu	Leu	
	1			5	10	
gat	cag	gac	ttg	ctg	ctg	220
Asp	Gln	Asp	Leu	Leu	Met	
	15			20	25	
agg	tcc	aaa	agc	tgg	aag	268
Arg	Ser	Lys	Ser	Trp	Lys	
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ggc	atg	aca	gtc	tgg	cat	316
Gly	Met	Thr	Val	Trp	His	
	45			50	55	
agc	ttc	tca	atc	tct	gat	364
Ser	Phe	Ser	Ile	Ser	Asp	
	60			65	70	
gag	ttg	ctg	cgt	agc	ctg	412
Glu	Leu	Leu	Arg	Ser	Leu	
			80		85	
acc	att	gtc	ttc	cat	ggc	460
Thr	Ile	Val	Phe	His	Gly	
		95			100	
agt	gtt	gag	gag	gcc	cag	508
Ser	Val	Glu	Glu	Ala	Gln	
	110			115	120	
gat	ctt	gtc	acc	agc	atg	556
Asp	Leu	Val	Thr	Ser	Met	
	125			130	135	
agc	gat	tgg	ttt	caa	cgt	604
Ser	Asp	Trp	Phe	Gln	Arg	
	140			145	150	
ttc	caa	gaa	gtt	cag	cgg	652
Phe	Gln	Glu	Val	Gln	Arg	
		160			165	
caa	gaa	tat	gcc	ttc	agt	700
Gln	Glu	Tyr	Ala	Phe	Ser	
		175			180	
gga	acc	ctg	gaa	gga	gaa	748
Gly	Thr	Leu	Glu	Gly	Glu	
		190			195	
aaa	cgt	gct	gag	gtg	cag	796
Lys	Arg	Ala	Glu	Val	Gln	
	205			210	215	

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ggc ttc ctc agc tac ctc tgc tct aag gat gga gac atc ttc aac cca Gly Phe Leu Ser Tyr Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro 270 275 280	988
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ttc atc tgc tct tct cat aac acc tac cta gtg ggg gac cag ctt tgc Phe Ile Cys Ser Ser His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys 300 305 310 315	1084
ggc cag agc agc gtc gag gga tat ata cgg gcc ctg aag cgg ggg tgc Gly Gln Ser Ser Val Glu Gly Tyr Ile Arg Ala Leu Lys Arg Gly Cys 320 325 330	1132
cgc tgc gtg gag gtg gat gta tgg gat gga cct agc ggg gaa cct gtc Arg Cys Val Glu Val Asp Val Trp Asp Gly Pro Ser Gly Glu Pro Val 335 340 345	1180
gtt tac cac gga cac acc ctg acc tcc cgc atc ctg ttc aaa gat gtc Val Tyr His Gly His Thr Leu Thr Ser Arg Ile Leu Phe Lys Asp Val 350 355 360	1228
gtg gcc aca gta gca cag tat gcc ttc cag aca tca gac tac cca gtc Val Ala Thr Val Ala Gln Tyr Ala Phe Gln Thr Ser Asp Tyr Pro Val 365 370 375	1276
atc ttg tcc ctg gag acc cac tgc agc tgg gag cag cag cag acc atg Ile Leu Ser Leu Glu Thr His Cys Ser Trp Glu Gln Gln Gln Thr Met 380 385 390 395	1324
gcc cgt cat ctg act gag atc ctg ggg gag cag ctg ctg agc acc acc Ala Arg His Leu Thr Glu Ile Leu Gly Glu Gln Leu Leu Ser Thr Thr 400 405 410	1372
ttg gat ggg gtg ctg ccc act cag ctg ccc tgc cct gag gag ctt cgg Leu Asp Gly Val Leu Pro Thr Gln Leu Pro Ser Pro Glu Glu Leu Arg 415 420 425	1420
agg aag atc ctg gtg aag ggg aag aag tta aca ctt gag gaa gac ctg Arg Lys Ile Leu Val Lys Gly Lys Lys Leu Thr Leu Glu Glu Asp Leu 430 435 440	1468
gaa tat gag gaa gag gaa gca gaa cct gag ttg gaa gag tca gaa ttg Glu Tyr Glu Glu Glu Glu Ala Glu Pro Glu Leu Glu Glu Ser Glu Leu 445 450 455	1516
gcg ctg gag tcc cag ttt gag act gag cct gag ccc cag gag cag aac Ala Leu Glu Ser Gln Phe Glu Thr Glu Pro Glu Pro Gln Glu Gln Asn 460 465 470 475	1564

ctt cag aat aag gac aaa aag aag aaa tcc aag ccc atc ttg tgt cca 1612
 Leu Gln Asn Lys Asp Lys Lys Lys Lys Ser Lys Pro Ile Leu Cys Pro
 480 485 490

gcc ctg tct tcc ctg gtt atc tac ttg aag tct gtc tca ttc cgc agc 1660
 Ala Leu Ser Ser Leu Val Ile Tyr Leu Lys Ser Val Ser Phe Arg Ser
 495 500 505

ttc aca cat tca aag gag cac tac cac ttc tac gag ata tca tct ttc 1708
 Phe Thr His Ser Lys Glu His Tyr His Phe Tyr Glu Ile Ser Ser Phe
 510 515 520

tct gaa acc aag gcc aag cgc ctg atc aag gag gct ggc aat gag ttt 1756
 Ser Glu Thr Lys Ala Lys Arg Leu Ile Lys Glu Ala Gly Asn Glu Phe
 525 530 535

gtg cag cac aat act cgg cag tta agc cgt gtg tat ccc agc ggc ctg 1804
 Val Gln His Asn Thr Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu
 540 545 550 555

agg aca ggc tct tcc atc tac aac ccg cag gga tac 1840
 Arg Thr Gly Ser Ile Tyr Asn Pro Gln Gly Tyr
 560 565

<210> 8
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 8

Met Ala Ser Leu Leu Gln Asp Gln Leu Thr Thr Asp Gln Asp Leu Leu
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 20 25 30

Lys Lys Leu Arg Tyr Phe Arg Leu Gln Asn Asp Gly Met Thr Val Trp
 35 40 45

His Ala Arg Gln Ala Arg Gly Ser Ala Lys Pro Ser Phe Ser Ile Ser
 50 55 60

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser
 65 70 75 80

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His
 85 90 95

Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala
 100 105 110

Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser
 115 120 125

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln
130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln
145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe
165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val
195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu
210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys
225 230 235 240

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp
245 250 255

Ser Gly Lys Leu Arg His Val Pro Ser Met Asp Gly Phe Leu Ser Tyr
260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile
275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser
290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val
305 310 315 320

Glu Gly Tyr Ile Arg Ala Leu Lys Arg Gly Cys Arg Cys Val Glu Val
325 330 335

Asp Val Trp Asp Gly Pro Ser Gly Glu Pro Val Val Tyr His Gly His
340 345 350

Thr Leu Thr Ser Arg Ile Leu Phe Lys Asp Val Val Ala Thr Val Ala
355 360 365

Gln Tyr Ala Phe Gln Thr Ser Asp Tyr Pro Val Ile Leu Ser Leu Glu
370 375 380

Thr His Cys Ser Trp Glu Gln Gln Gln Thr Met Ala Arg His Leu Thr
385 390 395 400

Glu Ile Leu Gly Glu Gln Leu Leu Ser Thr Thr Leu Asp Gly Val Leu
405 410 415

Pro Thr Gln Leu Pro Ser Pro Glu Glu Leu Arg Arg Lys Ile Leu Val
420 425 430

Lys Gly Lys Lys Leu Thr Leu Glu Glu Asp Leu Glu Tyr Glu Glu Glu
435 440 445

Glu Ala Glu Pro Glu Leu Glu Glu Ser Glu Leu Ala Leu Glu Ser Gln
450 455 460

Phe Glu Thr Glu Pro Glu Pro Gln Glu Gln Asn Leu Gln Asn Lys Asp
465 470 475 480

Lys Lys Lys Lys Ser Lys Pro Ile Leu Cys Pro Ala Leu Ser Ser Leu
485 490 495

Val Ile Tyr Leu Lys Ser Val Ser Phe Arg Ser Phe Thr His Ser Lys
500 505 510

Glu His Tyr His Phe Tyr Glu Ile Ser Ser Phe Ser Glu Thr Lys Ala
515 520 525

Lys Arg Leu Ile Lys Glu Ala Gly Asn Glu Phe Val Gln His Asn Thr
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Arg Gln Leu Ser Arg Val Tyr Pro Ser Gly Leu Arg Thr Gly Ser Ser
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Ile Tyr Asn Pro Gln Gly Tyr
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<211> 1384
<212> DNA
<213> Homo sapiens

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gaaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacac tggattgtct 180
cacacagaat ggaaatgtgg cttctgattc tgggtggcgtat tatgttccag agaaatgtga 240
attcagtaca tatgccaaact aaagctgtgg acccagaagc attcatgaat attagtga 300

tcatccaaca tcaaggttat cctgtgaggt aatatgaagt cgcaactgaa gatgggtata	360
tcctttctgt taacaggatt cctcgagccc tagtgcaacc taagaagaca ggttccaggc	420
ctgtgtgtgt actgcagcat ggcttagttg gaggtgctag caactggatt tccaacctgc	480
ccaacaatag cctgggcttc attctggcag atgctggttt tgacgtgtgg atggggaaca	540
gcaggggaaa cgctgtgtct cgaaaacaca agacactctc catagaccaa gatgagttct	600
gggctttcag ttatgatgag atggctaggt ttgaccttcc tgcagtata aactttattt	660
tgcagaaaaa gggccaggaa aagatctatt atgtcggcta ttcacagggc accaccatgg	720
gctttattgc attttccacc atgccagagc tggctcagaa aatcaaaatg tttttgctt	780
tagcacccat agccaactgtt aagcatgcaa aaagccccgg gaccaaattt ttgttgctgc	840
cagatatgat gatcaaggga ttgtttggca aaaaagaatt tctgtatcag accagatttc	900
tcagacaact tgttatttac ctttgtggcc aggtgattct tgatcagatt tgtagtaata	960
tcattgttact tctgggtgga ttcaacacca acaatatgaa catgagccga gcaagtgtat	1020
atgctgceca cactcttgct ggaacatctg tgcaaaatat tctacactgg agccaggcag	1080
tgaattctgg tgaactccgg gcatttgact gggggagtga gacaaaaat ctggaaaaat	1140
gcaatcagcc aactcctgta aggtacagag tcagagatat gacggtccct acagcaatgt	1200
ggacaggagg tcaggactgg ctttcaaatc cagaagacgt gaaaatgctg ctctctgagg	1260
tgaccaacct catctaccat aagaatatct ctgaatgggc tcattgtgat ttcattctggg	1320
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ccat	1384

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 <213> Homo sapiens

<220>
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agatgcaggc caagtacagc agcacgaggg acatgctgga tgatgatggg gacaccacc	179
atg agc ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc	227
Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro	
1 5 10 15	
cgg cgc aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc	275
Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala	
20 25 30	

ctg acc ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc	323
Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala	
35 40 45	
ctg ggg ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa	371
Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln	
50 55 60	
gac acc att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag	419
Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu	
65 70 75 80	
ttg caa tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag	467
Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln	
85 90 95	
cat gtg gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga ggc	515
His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly	
100 105 110	
tat aca aga aac atg gtg cca gca tct gct tct tct gag agc ctc agg	563
Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg	
115 120 125	
cag ctt cca cac atg ggg gaa agt gca gca gca cac agg tgc agc cct	611
Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro	
130 135 140	
tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat	659
Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr	
145 150 155 160	
aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa	707
Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu	
165 170 175	
aac tct acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc	755
Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala	
180 185 190	
gcg tct cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt	803
Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu	
195 200 205	
ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct	851
Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro	
210 215 220	
ttc act tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga	899
Phe Thr Ser Glu Leu Phe His Ile Ile Ile Val Thr Ser Pro Arg	
225 230 235 240	
agc aga gac tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac	947
Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp	
245 250 255	
tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg	995
Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val	
260 265 270	
aag cca gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac	1043
Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp	
275 280 285	

tga ttgcgcctct gcaactacaa atagcagagt gagccaggcg gtgccaaagc 1096
aagggctagt tgagacattg ggaatatggaa cataatcagg aaagactatc tctctgacta 1156
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gccgtttccc aacagggatg tcacttgata tgagaatctc aaatctcaat gccttataag 1636
cattccttcc tgtgtccatt aagactctga taattgtctc ccttccatag gaatttctcc 1696
caggaaagaa atatatcccc atctccgttt catatcagaa ctaccgtccc cgatatccccc 1756
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taattaaagg gaataccggg gaaaaaaaa aaaaagggg 1915

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<211> 288
<212> PRT
<213> Homo sapiens

<400> 11

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Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala
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Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala
35 40 45

Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln
50 55 60

Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu
65 70 75 80

Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln
85 90 95

His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly

100	105	110
Tyr Thr Arg Asn Met Val Pro Ala Ser Ser Glu Ser Leu Arg		
115	120	125
Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro		
130	135	140
Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr		
145	150	155
Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu		
165	170	175
Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala		
180	185	190
Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu		
195	200	205
Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro		
210	215	220
Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg		
225	230	235
Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp		
245	250	255
Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val		
260	265	270
Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp		
275	280	285

<210> 12
 <211> 2420
 <212> DNA
 <213> Homo sapiens

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 <223> n = a or c or g or t

<220>
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 <222> (200)..(2395)
 <223> Xaa = Unknown or other

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 gaagtccctag gactaatctc caggaccagc actcttctcc cagcccttag ggtcctgctc 180
 ggccaaggcc ttccctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc 232
 Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro
 1 5 10
 tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tgc tgc ttg ggg tct ccg 280
 Trp Gly Leu Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro
 15 20 25
 tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg 328
 Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg
 30 35 40
 ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag 376
 Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Gln Gly Arg Val Glu
 45 50 55
 ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg 424
 Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr
 60 65 70 75
 ctg cag gct gcc cac atc ctg tgc cgg gag ctg ggc ttc aca gag gcc 472
 Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala
 80 85 90
 aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc atc 520
 Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile
 95 100 105
 tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa 568
 Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu
 110 115 120
 tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag gat 616
 Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp
 125 130 135
 gct ggg gtc atc tgc aaa gac cag cgc ctg cct ggc ttc tgc gac tcc 664
 Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser
 140 145 150 155
 aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga att 712
 Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Glu Val Arg Ile
 160 165 170
 cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag ggg 760
 Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly
 175 180 185
 ctg gtg gaa gtc agg ctt cct gac ggc tgg tgc caa gtg tgc gac aaa 808
 Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys
 190 195 200
 ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc ttc 856
 Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly Phe
 205 210 215

ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc caa Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln 220 225 230 235	904
cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr 240 245 250	952
gag gcc cac ctc tcc ctg tgt tcc ctg gag ttc tat cgt gcc aat gac Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp 255 260 265	1000
acc gcc agg tgc cct ggg ggg gcc cct gca gtg gtg agc tgt gtg cca Thr Ala Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro 270 275 280	1048
ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag tgc Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser 285 290 295	1096
aag cct cag ggg gag gtc cgt gtc cgt cta aag ggc gcc gcc cac cct Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro 300 305 310 315	1144
gga gag gcc cgg gta gaa gtc ctg aag gcc agc aca tgg gcc aca gtc Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val 320 325 330	1192
tgt tac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg gag Cys Tyr Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu 335 340 345	1240
ctg gcc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg ggg Leu Gly Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly 350 355 360	1288
cag gcc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga cag Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln 365 370 375	1336
gag ctc tcc ctg tgg aag tgc ccc cac aag aac atc aca gct gag gat Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp 380 385 390 395	1384
tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac act Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr 400 405 410	1432
ggg gca gag acc agg gtc atc cat tct gtg tca cta cag atc cga ctc Gly Ala Glu Thr Arg Val Ile His Ser Val Ser Leu Gln Ile Arg Leu 415 420 425	1480
agt ggg gcc cgc agc caa cat gag ggg cga gtc gag gtg caa ata ggg Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val Gln Ile Gly 430 435 440	1528
gga cct ggg ccc ctt cgc tgg gcc ctc atc tgt ggg gat gac tgg ggg Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly 445 450 455	1576
acc ctg gag gcc atg gtg gcc tgt agg caa ctg ggt ctg gcc tac gcc Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala 460 465 470 475	1624

aac cac ggc ctg cag gag acc tgg tac tgg gac tct ggg aat ata aca Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr 480 485 490	1672
gag gtg gtg atg agt gga gtg cgc tgc aca ggg act gag ctg tcc ctg Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu 495 500 505	1720
gat cag tgt gcc cat cat ggc acc cac atc acc tgc aag agg aca ggg Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys Arg Thr Gly 510 515 520	1768
acc cgc ttc act gct gga gtc atc tgt tct gag gca tca gat ctg ttg Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu 525 530 535	1816
ctg cac tca gca ctg gtg cag gag acc gcc tac atc gaa gac cgg ccc Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro 540 545 550 555	1864
ctg cat atg ttg tac tgt gct gcg gaa gag aac tgc ctg gcc agc tca Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser 560 565 570	1912
gcc cgc tca gcc aac tgg ccc tat ggt cac cgg cgt ctg ctc cga ttc Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe 575 580 585	1960
tgc tcc cag atc cac aac ctg gga cga gct gac ttc agg ccc aag gct Cys Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala 590 595 600	2008
ggg cgc cac tcc tgg gtg tgg cac gag tgc cat ggg cat tac cac agc Gly Arg His Ser Trp Val Trp His Glu Cys His Gly His Tyr His Ser 605 610 615	2056
acg gac ttc ttc act cac tat gat atc ctc acc cca nat ggc acc aag Thr Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys 620 625 630 635	2104
gtg gct gag ggc cac aaa gct agt ttc tgt ctc gaa gac act gag tgt Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys 640 645 650	2152
cag gag gat gtc tcc aag cgg tat gag tgt gcc aac ttt gga gag caa Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln 655 660 665	2200
ggc atc act gtg ggd tgc tgg gat ctc tac cgg cat gac att gac tgt Gly Ile Thr Val Xaa Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys 670 675 680	2248
cag tgg att gac atc acg gat gtg aag cca gga aac tac att ctc cag Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln 685 690 695	2296
gtt gtc atc aac cca aac ttt gaa gta gca gag agb gac ttt acc aac Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Xaa Asp Phe Thr Asn 700 705 710 715	2344
aat gca atg aaa tgt aac tgc aaa tat gat gga cat aga atc tgg gtg Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His Arg Ile Trp Val 720 725 730	2392

cac macttgccac attggtgatg ccttc
His

2420

<210> 13
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<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> n = a or c or g or t

<400> 13

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
1 5 10 15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
180 185 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
260 265 270

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
290 295 300

Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Val Ile His Ser Val Ser Leu Gln Ile Arg Leu Ser Gly Gly Arg Ser
420 425 430

Gln His Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu
435 440 445

Arg Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met
450 455 460

Val Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln
465 470 475 480

Glu Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser
485 490 495

Gly Val Arg Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His
500 505 510

His Gly Thr His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala
515 520 525

Gly Val Ile Cys Ser Glu Ala Ser Asp Leu Leu Leu His Ser Ala Leu
530 535 540

Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr
545 550 555 560

Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn
565 570 575

Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe Cys Ser Gln Ile His
580 585 590

Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp
595 600 605

Val Trp His Glu Cys His Gly His Tyr His Ser Thr Asp Phe Phe Thr
610 615 620

His Tyr Asp Ile Leu Thr Pro Xaa Gly Thr Lys Val Ala Glu Gly His
625 630 635 640

Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser
645 650 655

Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Xaa
660 665 670

Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile
675 680 685

Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro
690 695 700

Asn Phe Glu Val Ala Glu Xaa Asp Phe Thr Asn Asn Ala Met Lys Cys
705 710 715 720

Asn Cys Lys Tyr Asp Gly His Arg Ile Trp Val His
725 730

<210> 14
<211> 2066
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (149) .. (2065)

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tccctccacc ttccacatcc tgctccaggc aggagaaggc tgactggctg gactcattga 120
gctgaagaat ttccagtgac atttgtaa atg acg ccg ctc gat tcc agg ctc 172
Met Thr Pro Leu Asp Ser Arg Leu
1 5
caa gcg gcc cct gcc gcc gcc gcc gcc ggg ccg aag gtg ccg ccg 220
Gln Ala Ala Pro Ala Ala Ala Ala Gly Pro Lys Val Pro Pro
10 15 20
agc agt ctc cag cgc agg ctt cct tac ccg gcg acc aca atg tcc gag 268
Ser Ser Leu Gln Arg Arg Leu Pro Tyr Arg Ala Thr Thr Met Ser Glu
25 30 35 40
ttt ctc ctc gcc tta ctc act ctc tcg gga tta ttg ccg att gcc agg 316
Phe Leu Leu Ala Leu Leu Thr Leu Ser Gly Leu Leu Pro Ile Ala Arg
45 50 55
gtg ctg acc gtg gga gcc gac cga gat cag cag ttg tgt gat cct ggt 364
Val Leu Thr Val Gly Ala Asp Arg Asp Gln Gln Leu Cys Asp Pro Gly
60 65 70
gaa ttt ctt tgc cac gat cac gtg act tgt gtc tcc cag agc tgg ctg 412
Glu Phe Leu Cys His Asp His Val Thr Cys Val Ser Gln Ser Trp Leu
75 80 85
tgt gat ggg gac cct gac tgc cct gat gat tca gac gag tct tta gat 460
Cys Asp Gly Asp Pro Asp Cys Pro Asp Asp Ser Asp Glu Ser Leu Asp
90 95 100
acc tgt ccc gag gag gta gaa atc aag tgc ccc ttg aat cac att gct 508
Thr Cys Pro Glu Glu Val Glu Ile Lys Cys Cys Leu Asn His Ile Ala
105 110 115 120
tgc ctt ggc acc aac aaa tgt gtt cat tta tcc cag ctg tgc aat ggt 556
Cys Leu Gly Thr Asn Lys Cys Val His Leu Ser Gln Leu Cys Asn Gly
125 130 135
gtc ttg gac tgc cca gat ggg tat gac gaa gga gta cat tgt cag gaa 604
Val Leu Asp Cys Pro Asp Gly Tyr Asp Glu Gly Val His Cys Gln Glu
140 145 150
ctg tta tcc aat tgc caa cag ctg aat tgt cag tat aaa tgt aca atg 652

Leu	Leu	Ser	Asn	Cys	Gln	Gln	Leu	Asn	Cys	Gln	Tyr	Lys	Cys	Thr	Met	
	155						160					165				
gtc	aga	aat	agt	aca	aga	tgt	tac	tgt	gag	gat	gga	ttc	gaa	ata	aca	700
Val	Arg	Asn	Ser	Thr	Arg	Cys	Tyr	Cys	Glu	Asp	Gly	Phe	Glu	Ile	Thr	
	170					175					180					
gaa	gat	ggg	aga	agc	tgt	aaa	gat	caa	gat	gaa	tgt	gct	gtt	tat	ggg	748
Glu	Asp	Gly	Arg	Ser	Cys	Lys	Asp	Gln	Asp	Glu	Cys	Ala	Val	Tyr	Gly	
	185				190				195					200		
aca	ggc	agc	cag	acc	tgc	aga	aac	aca	cat	gga	tcc	tac	act	tgc	agt	796
Thr	Gly	Ser	Gln	Thr	Cys	Arg	Asn	Thr	His	Gly	Ser	Tyr	Thr	Cys	Ser	
			205					210					215			
tgt	gtg	gaa	ggc	tac	cta	atg	cag	cca	gac	agc	aga	tct	tgc	aag	gct	844
Cys	Val	Glu	Gly	Tyr	Leu	Met	Gln	Pro	Asp	Ser	Arg	Ser	Cys	Lys	Ala	
		220					225					230				
aaa	att	gaa	cct	aca	gat	aga	cca	cgt	ata	cta	tta	att	gca	aat	ttt	892
Lys	Ile	Glu	Pro	Thr	Asp	Arg	Pro	Arg	Ile	Leu	Leu	Ile	Ala	Asn	Phe	
	235					240					245					
gaa	tca	att	gag	gtt	ttc	tat	ctt	aat	gga	agt	aaa	att	gca	act	cta	940
Glu	Ser	Ile	Glu	Val	Phe	Tyr	Leu	Asn	Gly	Ser	Lys	Ile	Ala	Thr	Leu	
	250				255						260					
agc	tca	gtc	aat	gga	aat	gaa	att	cat	act	ctg	gat	ttt	att	tat	aat	988
Ser	Ser	Val	Asn	Gly	Asn	Glu	Ile	His	Thr	Leu	Asp	Phe	Ile	Tyr	Asn	
	265				270				275						280	
gaa	gat	gtg	att	tgt	tgg	att	gaa	tca	aga	gaa	tct	tca	aat	caa	ctc	1036
Glu	Asp	Val	Ile	Cys	Trp	Ile	Glu	Ser	Arg	Glu	Ser	Ser	Asn	Gln	Leu	
				285					290					295		
aaa	tgt	atc	cag	ata	aca	aaa	gca	gga	gga	tta	aca	gat	gaa	tgg	aca	1084
Lys	Cys	Ile	Gln	Ile	Thr	Lys	Ala	Gly	Gly	Leu	Thr	Asp	Glu	Trp	Thr	
		300					305						310			
atc	aat	att	ctt	caa	tcc	ttc	cac	aat	gtg	caa	caa	atg	gcg	att	gac	1132
Ile	Asn	Ile	Leu	Gln	Ser	Phe	His	Asn	Val	Gln	Gln	Met	Ala	Ile	Asp	
	315					320						325				
tgg	ctc	act	cga	aat	ctc	tat	ttt	gtg	gac	cat	gtc	ggg	gac	cgg	atc	1180
Trp	Leu	Thr	Arg	Asn	Leu	Tyr	Phe	Val	Asp	His	Val	Gly	Asp	Arg	Ile	
	330				335						340					
ttt	gtt	tgt	aat	tcc	aac	ggg	tct	gta	tgt	gtc	acc	ctg	att	gat	ctg	1228
Phe	Val	Cys	Asn	Ser	Asn	Gly	Ser	Val	Cys	Val	Thr	Leu	Ile	Asp	Leu	
	345				350				355						360	
gag	ctt	cac	aat	cct	aaa	gca	ata	gca	gta	gat	cca	ata	gca	gga	aaa	1276
Glu	Leu	His	Asn	Pro	Lys	Ala	Ile	Ala	Val	Asp	Pro	Ile	Ala	Gly	Lys	
			365						370				375			
ctt	ttc	ttt	act	gac	tac	ggg	aat	gtc	gcc	aaa	gtg	gag	aga	tgt	gac	1324
Leu	Phe	Phe	Thr	Asp	Tyr	Gly	Asn	Val	Ala	Lys	Val	Glu	Arg	Cys	Asp	
		380				385						390				
atg	gat	ggg	atg	aac	cga	aca	agg	ata	att	gat	tca	aag	aca	gag	cag	1372
Met	Asp	Gly	Met	Asn	Arg	Thr	Arg	Ile	Ile	Asp	Ser	Lys	Thr	Glu	Gln	
	395					400					405					

cca gct gca ctg gca cta gac cta gtc aac aaa ttg gtt tac tgg gta Pro Ala Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val 410 415 420	1420
gat ctt tac ttg gac tat gtg gga gta gtg gac tat caa gga aaa aat Asp Leu Tyr Leu Asp Tyr Val Gly Val Val Asp Tyr Gln Gly Lys Asn 425 430 435 440	1468
aga cac act gtc att caa ggc aga caa gtc aga cat ctt tat ggt ata Arg His Thr Val Ile Gln Gly Arg Gln Val Arg His Leu Tyr Gly Ile 445 450 455	1516
act gtg ttt gaa gat tat ttg tat gca acc aat tct gat aac tac aat Thr Val Phe Glu Asp Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Tyr Asn 460 465 470	1564
atc gta agg ata aac cga ttt aat ggg act gat att cac tca tta att Ile Val Arg Ile Asn Arg Phe Asn Gly Thr Asp Ile His Ser Leu Ile 475 480 485	1612
aaa att gag aat gct tgg gga atc cga att tat caa aaa aga act caa Lys Ile Glu Asn Ala Trp Gly Ile Arg Ile Tyr Gln Lys Arg Thr Gln 490 495 500	1660
cca aca gtc aga agc cat gca tgt gaa gtc gat cca tat gga atg cca Pro Thr Val Arg Ser His Ala Cys Glu Val Asp Pro Tyr Gly Met Pro 505 510 515 520	1708
ggg ggc tgt tca cac atc tgt cta ctc agc agc agt tac aaa act cgg Gly Gly Cys Ser His Ile Cys Leu Leu Ser Ser Ser Tyr Lys Thr Arg 525 530 535	1756
act tgt cgc tgc agg act ggc ttc aac ttg gga agt gat ggc agg tca Thr Cys Arg Cys Arg Thr Gly Phe Asn Leu Gly Ser Asp Gly Arg Ser 540 545 550	1804
tgc aaa aga cca aag aat gag ttg ttc ctc ttt tat ggg aaa gga cgc Cys Lys Arg Pro Lys Asn Glu Leu Phe Leu Phe Tyr Gly Lys Gly Arg 555 560 565	1852
cca gga att gtt aga gga atg gac ttg aat acc aag ata gct gat gaa Pro Gly Ile Val Arg Gly Met Asp Leu Asn Thr Lys Ile Ala Asp Glu 570 575 580	1900
tac atg atc ccc ata gaa aat ctg gta aac cct cgt gct tta gac ttt Tyr Met Ile Pro Ile Glu Asn Leu Val Asn Pro Arg Ala Leu Asp Phe 585 590 595 600	1948
cac gca gaa acc aat tac atc tac ttt gct gac acc acc agt ttc cta His Ala Glu Thr Asn Tyr Ile Tyr Phe Ala Asp Thr Thr Ser Phe Leu 605 610 615	1996
att ggc cgg cag aag ata gat ggc aca gag aga gaa acc atc ctg aaa Ile Gly Arg Gln Lys Ile Asp Gly Thr Gln Arg Glu Thr Ile Leu Lys 620 625 630	2044
gat gat ctg gat aat gta gag g Asp Asp Leu Asp Asn Val Glu 635	2066

<212> PRT
<213> Homo sapiens

<400> 15

Met Thr Pro Leu Asp Ser Arg Leu Gln Ala Ala Pro Ala Ala Ala Ala
1 5 10 15

Ala Ala Gly Pro Lys Val Pro Pro Ser Ser Leu Gln Arg Arg Leu Pro
20 25 30

Tyr Arg Ala Thr Thr Met Ser Glu Phe Leu Leu Ala Leu Leu Thr Leu
35 40 45

Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg
50 55 60

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val
65 70 75 80

Thr Cys Val Ser Gln Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro
85 90 95

Asp Asp Ser Asp Glu Ser Leu Asp Thr Cys Pro Glu Glu Val Glu Ile
100 105 110

Lys Cys Pro Leu Asn His Ile Ala Cys Leu Gly Thr Asn Lys Cys Val
115 120 125

His Leu Ser Gln Leu Cys Asn Gly Val Leu Asp Cys Pro Asp Gly Tyr
130 135 140

Asp Glu Gly Val His Cys Gln Glu Leu Leu Ser Asn Cys Gln Gln Leu
145 150 155 160

Asn Cys Gln Tyr Lys Cys Thr Met Val Arg Asn Ser Thr Arg Cys Tyr
165 170 175

Cys Glu Asp Gly Phe Glu Ile Thr Glu Asp Gly Arg Ser Cys Lys Asp
180 185 190

Gln Asp Glu Cys Ala Val Tyr Gly Thr Gly Ser Gln Thr Cys Arg Asn
195 200 205

Thr His Gly Ser Tyr Thr Cys Ser Cys Val Glu Gly Tyr Leu Met Gln
210 215 220

Pro Asp Ser Arg Ser Cys Lys Ala Lys Ile Glu Pro Thr Asp Arg Pro
225 230 235 240

Arg Ile Leu Leu Ile Ala Asn Phe Glu Ser Ile Glu Val Phe Tyr Leu
245 250 255

Asn Gly Ser Lys Ile Ala Thr Leu Ser Ser Val Asn Gly Asn Glu Ile
260 265 270

His Thr Leu Asp Phe Ile Tyr Asn Glu Asp Val Ile Cys Trp Ile Glu
275 280 285

Ser Arg Glu Ser Ser Asn Gln Leu Lys Cys Ile Gln Ile Thr Lys Ala
290 295 300

Gly Gly Leu Thr Asp Glu Trp Thr Ile Asn Ile Leu Gln Ser Phe His
305 310 315 320

Asn Val Gln Gln Met Ala Ile Asp Trp Leu Thr Arg Asn Leu Tyr Phe
325 330 335

Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser
340 345 350

Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile
355 360 365

Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn
370 375 380

Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg
385 390 395 400

Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu
405 410 415

Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly
420 425 430

Val Val Asp Tyr Gln Gly Lys Asn Arg His Thr Val Ile Gln Gly Arg
435 440 445

Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr
450 455 460

Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn
465 470 475 480

Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile
485 490 495

Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr Val Arg Ser His Ala Cys
500 505 510

Glu Val Asp Pro Tyr Gly Met Pro Gly Gly Cys Ser His Ile Cys Leu
515 520 525

Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys Arg Cys Arg Thr Gly Phe
530 535 540

Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys Arg Pro Lys Asn Glu Leu
545 550 555 560

Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly Ile Val Arg Gly Met Asp
565 570 575

Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu
580 585 590

Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr
595 600 605

Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly Arg Gln Lys Ile Asp Gly
610 615 620

Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp Leu Asp Asn Val Glu
625 630 635

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<211> 1333
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (280)..(1323)

<400> 16
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tggaggaggc ccgcagcga catggaggga gctgcttgc tgaagtcct tgcctctgc 120
atctggaacc aaaatcactt ccggaattg accaactggt agactcgct agaggggaag 180
cattgtgtcc tagttgaggc taacagtcag tatccagcct caacattcag cagaggeccc 240
agatcagcgt ctgagccagg ccaacaatga ccaaggagg atg gga tcc tgg gtc 294
Met Gly Ser Trp Val
1 5

cag ctc atc aca agc gtc ggg gtc cag caa aac cat cca ggc tgg aca 342
Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn His Pro Gly Trp Thr
10 15 20

gtg gct gga cag ttc caa gaa aag aaa cgc ttc act gaa gaa gtc att Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe Thr Glu Glu Val Ile 25 30 35	390
gaa tac ttc cag aag aaa gtt agc cca gtg cat ctg aaa atc ctg ctg Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His Leu Lys Ile Leu Leu 40 45 50	438
act agc gat gaa gcc tgg aag aga ttc gtg cgt gtg gct gaa ttg ccc Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg Val Ala Glu Leu Pro 55 60 65	486
agg gaa gaa gca gat gct ctc tat gaa gct ctg aag aat ctt aca cca Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu Lys Asn Leu Thr Pro 70 75 80 85	534
tat gtg gct att gag gac aaa gac atg cag caa aaa gaa cag cag ttt Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln Lys Glu Gln Gln Phe 90 95 100	582
agg gag tgg ttt ttg aaa gag ttt cct caa atc aga tgg aag att cag Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile Arg Trp Lys Ile Gln 105 110 115	630
gag tcc ata gaa agg ctt cgt gtc att gca aat gag att gaa aag gtc Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn Glu Ile Glu Lys Val 120 125 130	678
cac aga ggc tgc gtc atc gcc aat gtg gtg tct ggc tcc act ggc atc His Arg Gly Cys Val Ile Ala Asn Val Val Ser Gly Ser Thr Gly Ile 135 140 145	726
ctg tct gtc att ggc gtt atg ttg gca cca ttt aca gca ggg ctg agc Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe Thr Ala Gly Leu Ser 150 155 160 165	774
ctg agc att act gca gct ggg gta ggg ctg gga ata gca tct gcc acg Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly Ile Ala Ser Ala Thr 170 175 180	822
gct ggg atc gcc tcc agc atc gtg gag aac aca tac aca agg tca gca Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr Tyr Thr Arg Ser Ala 185 190 195	870
gaa ctc aca gcc agc agg ctg act gca acc agc act gac caa ttg gag Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser Thr Asp Gln Leu Glu 200 205 210	918
gca tta agg gac att ctg cgt gac atc aca ccc aat gtg ctt tct ttt Ala Leu Arg Asp Ile Leu Arg Asp Ile Thr Pro Asn Val Leu Ser Phe 215 220 225	966
gca ctt gat ttt gac gaa gcc aca aaa atg att gcg aat gat gtc cat Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile Ala Asn Asp Val His 230 235 240 245	1014
aca ctc agg aga tct aaa gcc act gtt gga cgc cct ttg att gct tgg Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg Pro Leu Ile Ala Trp 250 255 260	1062
cga tat gta cct ata aat gtt gtt gag aca ctg aga aca cgt ggg gcc Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu Arg Thr Arg Gly Ala 265 270 275	1110

ccc acc cgg ata gtg aga aaa gta gcc cgg aac ctg ggc aag gcc act 1158
Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn Leu Gly Lys Ala Thr
280 285 290

tca ggt gtc ctt gtt gtg ctg gat gta gtc aac ctt gtg caa gac tca 1206
Ser Gly Val Leu Val Val Leu Asp Val Val Asn Leu Val Gln Asp Ser
295 300 305

ctg gac ttg cac aag ggg gca aaa tcc gag tct gct gag tgg ctg agg 1254
Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser Ala Glu Ser Leu Arg
310 315 320 325

cag tgg gct cag gag ctg gag gag aat ctc aat gag ctc acc cat atc 1302
Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn Glu Leu Thr His Ile
330 335 340

cat cag agt cta aaa gca ggc taggccaat 1333
His Gln Ser Leu Lys Ala Gly
345

<210> 17
<211> 348
<212> PRT
<213> Homo sapiens

<400> 17

Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn
1 5 10 15

His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
20 25 30

Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
35 40 45

Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
50 55 60

Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
65 70 75 80

Lys Asn Leu Thr Pro Tyr Val Ala Ile Glu Asp Lys Asp Met Gln Gln
85 90 95

Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
100 105 110

Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn
115 120 125

Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser
130 135 140

Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe
145 150 155 160

Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
165 170 175

Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr
180 185 190

Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser
195 200 205

Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu Arg Asp Ile Thr Pro
210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
225 230 235 240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
260 265 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
290 295 300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser
305 310 315 320

Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn
325 330 335

Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly
340 345

<210> 18
<211> 1490
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (151)..(1170)

<400> 18
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aggcacagct cacagacaca ggaacacag gactgctatt ctgctctcct gcccacgggtg	120
atctgggtgcc agctgggtgga acagtgggtg atg gcg tcc ctg ctg caa gac cag Met Ala Ser Leu Leu Gln Asp Gln 1 5	174
ctg acc act gat cag gac ttg ctg ctg atg cag gaa ggc atg ccg atg Leu Thr Thr Asp Gln Asp Leu Leu Leu Met Gln Gly Met Pro Met 10 15 20	222
cgc aag gtg agg tcc aaa agc tgg aag aag cta aga tac ttc aga ctt Arg Lys Val Arg Ser Lys Ser Trp Lys Lys Leu Arg Tyr Phe Arg Leu 25 30 35 40	270
cag aat gac ggc atg aca gtc tgg cat gca cgg cag gcc agg ggc agt Gln Asn Asp Gly Met Thr Val Trp His Ala Arg Gln Ala Arg Gly Ser 45 50 55	318
gcc aag ccc agc ttc tca atc tct gat gtg gag aca ata cgt aat ggc Ala Lys Pro Ser Phe Ser Ile Ser Asp Val Glu Thr Ile Arg Asn Gly 60 65 70	366
cat gat tcc gag ttg ctg cgt agc ctg gca gag gag ctc ccc ctg gag His Asp Ser Glu Leu Leu Arg Ser Leu Ala Glu Glu Leu Pro Leu Glu 75 80 85	414
cag ggc ttc acc att gtc ttc cat ggc cgc cgc tcc aac ctg gac ctg Gln Gly Phe Thr Ile Val Phe His Gly Arg Arg Ser Asn Leu Asp Leu 90 95 100	462
atg gcc aac agt gtt gag gag gcc cag ata tgg atg cga ggg ctc cag Met Ala Asn Ser Val Glu Glu Ala Gln Ile Trp Met Arg Gly Leu Gln 105 110 115 120	510
ctg ttg gtg gat ctt gtc acc agc atg gac cat cag gag cgc ctg gac Leu Leu Val Asp Leu Val Thr Ser Met Asp His Gln Glu Arg Leu Asp 125 130 135	558
caa tgg ctg agc gat tgg ttt caa cgt gga gac aaa aat cag gat ggt Gln Trp Leu Ser Asp Trp Phe Gln Arg Gly Asp Lys Asn Gln Asp Gly 140 145 150	606
aag atg agt ttc caa gaa gtt cag cgg tta ttg cac cta atg aat gtg Lys Met Ser Phe Gln Glu Val Gln Arg Leu Leu His Leu Met Asn Val 155 160 165	654
gaa atg gac caa gaa tat gcc ttc agt ctt ttt cag gca gca gac acg Glu Met Asp Gln Glu Tyr Ala Phe Ser Leu Phe Ala Ala Asp Thr 170 175 180	702
tcc cag tct gga acc ctg gaa gga gaa gaa ttc gta cag ttc tat aag Ser Gln Ser Gly Thr Leu Glu Gly Glu Glu Phe Val Gln Phe Tyr Lys 185 190 195 200	750
gca ttg act aaa cgt gct gag gtg cag gaa ctg ttt gaa agt ttt tca Ala Leu Thr Lys Arg Ala Glu Val Gln Glu Leu Phe Glu Ser Phe Ser 205 210 215	798
gct gat ggg cag aag ctg act ctg ctg gaa ttt ttg gat ttc ctc caa Ala Asp Gly Gln Lys Leu Thr Leu Leu Glu Phe Leu Asp Phe Leu Gln 220 225 230	846
gag gag cag aag gag aga gac tgc acc tct gag ctt gct ctg gaa ctc	894

Glu	Glu	Gln	Lys	Glu	Arg	Asp	Cys	Thr	Ser	Glu	Leu	Ala	Leu	Glu	Leu		
	235						240					245					
att	gac	cgc	tat	gaa	cct	tca	gac	agt	ggc	aaa	ctg	cgg	cat	gtg	ctg	942	
Ile	Asp	Arg	Tyr	Glu	Pro	Ser	Asp	Ser	Gly	Lys	Leu	Arg	His	Val	Leu		
	250					255					260						
agt	atg	gat	ggc	ttc	ctc	agc	tac	ctc	tgc	tct	aag	gat	gga	gac	atc	990	
Ser	Met	Asp	Gly	Phe	Leu	Ser	Tyr	Leu	Cys	Ser	Lys	Asp	Gly	Asp	Ile		
	265				270				275					280			
ttc	aac	cca	gcc	tgc	ctc	ccc	atc	tat	cag	gat	atg	act	caa	ccc	ctg	1038	
Phe	Asn	Pro	Ala	Cys	Leu	Pro	Ile	Tyr	Gln	Asp	Met	Thr	Gln	Pro	Leu		
			285					290					295				
aac	cac	tac	ttc	atc	tgc	tct	tct	cat	aac	acc	tac	cta	gtg	ggg	gac	1086	
Asn	His	Tyr	Phe	Ile	Cys	Ser	Ser	His	Asn	Thr	Tyr	Leu	Val	Gly	Asp		
			300					305					310				
cag	ctt	tgc	ggc	cag	agc	agc	gtc	gag	gga	tat	ata	cgg	tgc	agt	ggc	1134	
Gln	Leu	Cys	Gly	Gln	Ser	Ser	Val	Glu	Gly	Tyr	Ile	Arg	Cys	Ser	Gly		
		315					320					325					
ggc	aga	gaa	ggg	gtc	caa	ctc	atg	aga	ggg	acc	atg	tagaaa	agtg			1180	
Gly	Arg	Glu	Gly	Val	Gln	Leu	Met	Arg	Gly	Thr	Met						
		330				335					340						
aggggagctg	tcagtgctca	acagattggg	acagtggtgt	ggggggttag	gggctgagga											1240	
gcctctggata	ccagagacac	ttggaggaga	tattgaagac	tggtgggaga	atggtaatga											1300	
aaccctatgg	gtcaatggaa	cttctcttct	acaagctatg	aaactctctc	ggaactcaga											1360	
ggcctgaca	gatttatatt	taacaaatta	ataaacagat	tgtaaattgg	aaggcaatag											1420	
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ctttacttgg																1490	

<210> 19
 <211> 340
 <212> PRT
 <213> Homo sapiens

<400> 19

Met	Ala	Ser	Leu	Leu	Gln	Asp	Gln	Leu	Thr	Thr	Asp	Gln	Asp	Leu	Leu		
1				5					10					15			

Leu	Met	Gln	Glu	Gly	Met	Pro	Met	Arg	Lys	Val	Arg	Ser	Lys	Ser	Trp		
		20					25						30				

Lys	Lys	Leu	Arg	Tyr	Phe	Arg	Leu	Gln	Asn	Asp	Gly	Met	Thr	Val	Trp		
		35					40					45					

His	Ala	Arg	Gln	Ala	Arg	Gly	Ser	Ala	Lys	Pro	Ser	Phe	Ser	Ile	Ser		
	50					55					60						

Asp Val Glu Thr Ile Arg Asn Gly His Asp Ser Glu Leu Leu Arg Ser
65 70 75 80

Leu Ala Glu Glu Leu Pro Leu Glu Gln Gly Phe Thr Ile Val Phe His
85 90 95

Gly Arg Arg Ser Asn Leu Asp Leu Met Ala Asn Ser Val Glu Glu Ala
100 105 110

Gln Ile Trp Met Arg Gly Leu Gln Leu Leu Val Asp Leu Val Thr Ser
115 120 125

Met Asp His Gln Glu Arg Leu Asp Gln Trp Leu Ser Asp Trp Phe Gln
130 135 140

Arg Gly Asp Lys Asn Gln Asp Gly Lys Met Ser Phe Gln Glu Val Gln
145 150 155 160

Arg Leu Leu His Leu Met Asn Val Glu Met Asp Gln Glu Tyr Ala Phe
165 170 175

Ser Leu Phe Gln Ala Ala Asp Thr Ser Gln Ser Gly Thr Leu Glu Gly
180 185 190

Glu Glu Phe Val Gln Phe Tyr Lys Ala Leu Thr Lys Arg Ala Glu Val
195 200 205

Gln Glu Leu Phe Glu Ser Phe Ser Ala Asp Gly Gln Lys Leu Thr Leu
210 215 220

Leu Glu Phe Leu Asp Phe Leu Gln Glu Glu Gln Lys Glu Arg Asp Cys
225 230 235 240

Thr Ser Glu Leu Ala Leu Glu Leu Ile Asp Arg Tyr Glu Pro Ser Asp
245 250 255

Ser Gly Lys Leu Arg His Val Leu Ser Met Asp Gly Phe Leu Ser Tyr
260 265 270

Leu Cys Ser Lys Asp Gly Asp Ile Phe Asn Pro Ala Cys Leu Pro Ile
275 280 285

Tyr Gln Asp Met Thr Gln Pro Leu Asn His Tyr Phe Ile Cys Ser Ser
290 295 300

His Asn Thr Tyr Leu Val Gly Asp Gln Leu Cys Gly Gln Ser Ser Val
305 310 315 320

Glu Gly Tyr Ile Arg Cys Ser Gly Gly Arg Glu Gly Val Gln Leu Met
325 330 335

Arg Gly Thr Met
340

<210> 20
<211> 2035
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (189)..(1415)

<400> 20
ccaactaagc ttgcctaatt tgcttcagaa ttggaagagg gaattgcagc aggaaaatat 60
gtgaagaggt tttaaaccca caaattcttc ttactttaga attagttgtt acattggcag 120
gaaaaataa atgcagatgt tggaccatgt tggaaacctt gtcaagacag tggattgtct 180
cacacaga atg gaa atg tgg ctt ctg att ctg gtg gcg tat atg ttc cag 230
Met Glu Met Trp Leu Leu Ile Leu Val Ala Tyr Met Phe Gln
1 5 10
aga aat gtg aat tca gta cat atg cca act aaa gct gtg gac cca gaa 278
Arg Asn Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu
15 20 25 30
gca ttc atg aat att agt gaa atc atc caa cat caa ggc tat ccc tgt 326
Ala Phe Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys
35 40 45
gag gaa tat gaa gtc gca act gaa gat ggg tat atc ctt tct gtt aac 374
Glu Glu Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn
50 55 60
agg att cct cga ggc cta gtg caa cct aag aag aca ggt tcc agg cct 422
Arg Ile Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro
65 70 75
gtg gtg tta ctg cag cat ggc cta gtt gga ggt gct agc aac tgg att 470
Val Val Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile
80 85 90
tcc aac ctg ccc aac aat agc ctg ggc ttc att ctg gca gat gct ggt 518
Ser Asn Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly
95 100 105 110
ttt gac gtg tgg atg ggg aac agc agg gga aac gcc tgg tct cga aaa 566
Phe Asp Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys
115 120 125
cac aag aca ctc tcc ata gac caa gat gag ttc tgg gct ttc agt tat 614
His Lys Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr
130 135 140
gat gag atg gct agg ttt gac ctt cct gca gtg ata aac ttt att ttg 662
Asp Glu Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu
145 150 155

cag aaa acg ggc cag gaa aag atc tat tat gtc ggc tat tca cag ggc Gln Lys Thr Gly Gln Gln Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly 160 165 170	710
acc acc atg ggc ttt att gca ttt tcc acc atg cca gag ctg gct cag Thr Thr Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln 175 180 185 190	758
aaa atc aaa atg tat ttt gct tta gca ccc ata gcc act gtt aag cat Lys Ile Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His 195 200 205	806
gca aaa agc ccc ggc acc aaa ttt ttg ttg ctg cca gat atg atg atc Ala Lys Ser Pro Gly Thr Lys Phe Leu Leu Leu Pro Asp Met Met Ile 210 215 220	854
aag gga ttg ttt ggc aaa aaa gaa ttt ctg tat cag acc aga ttt ctc Lys Gly Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu 225 230 235	902
aga caa ctt gtt att tac ctt tgt ggc cag gtg att ctt gat cag att Arg Gln Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile 240 245 250	950
tgt agt aat atc atg tta ctt ctg ggt gga ttc aac acc aat atg Cys Ser Asn Ile Met Leu Leu Leu Gly Gly Phe Asn Thr Asn Asn Met 255 260 265 270	998
aac atg agc cga gca agt gta tat gct gcc cac act ctt gct gga aca Asn Met Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr 275 280 285	1046
tct gtg caa aat att cta cac tgg agc cag gca gtg aat tct ggt gaa Ser Val Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu 290 295 300	1094
ctc cgg gca ttt gac tgg ggg agt gag acc aaa aat ctg gaa aaa tgc Leu Arg Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys 305 310 315	1142
aat cag cca act cct gta agg tac aga gtc aga gat atg acg gtc cct Asn Gln Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro 320 325 330	1190
aca gca atg tgg aca gga ggt cag gac tgg ctt tca aat cca gaa gac Thr Ala Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp 335 340 345 350	1238
gtg aaa atg ctg ctc tct gag gtg acc aac ctc atc tac cat aag aat Val Lys Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn 355 360 365	1286
att cct gaa tgg gct cat gtg gat ttc atc tgg ggt ttg gat gct cct Ile Pro Glu Trp Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro 370 375 380	1334
cac cgt atg tac aat gaa atc atc cat ctg atg cag cag gag gag acc His Arg Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr 385 390 395	1382
aac ctt tcc cag gga cgg tgt gag gcc gta ttg tgaagcatct gacactgacg Asn Leu Ser Gln Gly Arg Cys Glu Ala Val Leu 400 405	1435

atcttaggac aacctcctga gggatggggc taggacccat gaaggcagaa ttatggagag 1495
 cagagacctt gtatacattt ttcagattcc ctgcacttgg cactaaatcc gacacttaca 1555
 ttacattttt tttctgttaa attaaagtac ttattaggta aatagaggtt ttgtatgcta 1615
 ttatatattc taccatcttg aagggttagt ttacotgat agccagaaaa tatctagaca 1675
 ttctctatat cattcaggta aatctcttta aaacacctat tgttttttct ataagccata 1735
 tttttggagc actaaagtaa aatggcaaat tgggacagat attgagggtct ggagtctgtg 1795
 gattattggt gactttgaca aaataagcta gacattttca ccttgttgcc acagagacat 1855
 aacctacct caggaagctg agctgcttta aggacaacaa caacaaaatc agtggttacag 1915
 tatggatgaa atctatgtta agcattctca gaataaggcc aagttttata gttgcatttc 1975
 aggaagaaaa attttatagg atgtttatga gttctccaat aaatgcattc tgcattacat 2035

<210> 21
 <211> 409
 <212> PRT
 <213> Homo sapiens

<400> 21

Met Glu Met Trp Leu Ile Leu Val Ala Tyr Met Phe Gln Arg Asn
 1 5 10 15

Val Asn Ser Val His Met Pro Thr Lys Ala Val Asp Pro Glu Ala Phe
 20 25 30

Met Asn Ile Ser Glu Ile Ile Gln His Gln Gly Tyr Pro Cys Glu Glu
 35 40 45

Tyr Glu Val Ala Thr Glu Asp Gly Tyr Ile Leu Ser Val Asn Arg Ile
 50 55 60

Pro Arg Gly Leu Val Gln Pro Lys Lys Thr Gly Ser Arg Pro Val Val
 65 70 75 80

Leu Leu Gln His Gly Leu Val Gly Gly Ala Ser Asn Trp Ile Ser Asn
 85 90 95

Leu Pro Asn Asn Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp
 100 105 110

Val Trp Met Gly Asn Ser Arg Gly Asn Ala Trp Ser Arg Lys His Lys
 115 120 125

Thr Leu Ser Ile Asp Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu
 130 135 140

Met Ala Arg Phe Asp Leu Pro Ala Val Ile Asn Phe Ile Leu Gln Lys
145 150 155 160

Thr Gly Gln Glu Lys Ile Tyr Tyr Val Gly Tyr Ser Gln Gly Thr Thr
165 170 175

Met Gly Phe Ile Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Lys Ile
180 185 190

Lys Met Tyr Phe Ala Leu Ala Pro Ile Ala Thr Val Lys His Ala Lys
195 200 205

Ser Pro Gly Thr Lys Phe Leu Leu Leu Pro Asp Met Met Ile Lys Gly
210 215 220

Leu Phe Gly Lys Lys Glu Phe Leu Tyr Gln Thr Arg Phe Leu Arg Gln
225 230 235 240

Leu Val Ile Tyr Leu Cys Gly Gln Val Ile Leu Asp Gln Ile Cys Ser
245 250 255

Asn Ile Met Leu Leu Leu Gly Gly Phe Asn Thr Asn Asn Met Asn Met
260 265 270

Ser Arg Ala Ser Val Tyr Ala Ala His Thr Leu Ala Gly Thr Ser Val
275 280 285

Gln Asn Ile Leu His Trp Ser Gln Ala Val Asn Ser Gly Glu Leu Arg
290 295 300

Ala Phe Asp Trp Gly Ser Glu Thr Lys Asn Leu Glu Lys Cys Asn Gln
305 310 315 320

Pro Thr Pro Val Arg Tyr Arg Val Arg Asp Met Thr Val Pro Thr Ala
325 330 335

Met Trp Thr Gly Gly Gln Asp Trp Leu Ser Asn Pro Glu Asp Val Lys
340 345 350

Met Leu Leu Ser Glu Val Thr Asn Leu Ile Tyr His Lys Asn Ile Pro
355 360 365

Glu Trp Ala His Val Asp Phe Ile Trp Gly Leu Asp Ala Pro His Arg
370 375 380

Met Tyr Asn Glu Ile Ile His Leu Met Gln Gln Glu Glu Thr Asn Leu
385 390 395 400

Ser Gln Gly Arg Cys Glu Ala Val Leu
405

<210> 22
<211> 2224
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> n = a or c or g or t

<220>
<221> CDS
<222> (82)..(921)
<223> Xaa = Unknown or other

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<400> 22
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ctcaccgctg taggaatcca g atg cag gcc aag tac agc agc acg agg gac      111
                        Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp
                        1                    5                10

atg ctg gat gat gat ggg gac acc acc atg agc ctg cat tct caa gcc      159
Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala
                        15                20                25

tct gcc aca act cgg cat cca gag ccc cgg cgc aca gag cac agg gct      207
Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala
                        30                35                40

ccc tct tca acg tgg cga cca gtg gcc ctg acc ctg ctg act ttg tgc      255
Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys
                        45                50                55

ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg ctt ttg ttt ttt cag      303
Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln
                        60                65                70

tac tac cag ctc tcc aat act ggt caa gac acc att tct caa atg gaa      351
Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu
75                        80                        85                90

gaa aga tta gga aat acg tcc caa gag ttg caa tct ctt caa gtc cag      399
Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln
                        95                100                105

aat ata aag ctt gca gga agt ctg cag cat gtg gct gaa aaa ctc tgt      447
Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys
110                115                120

cgt gag ctg tat aac aaa gct gga gca cac agg tgc agc cct tgt aca      495
Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser Pro Cys Thr
125                130                135

gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac      543
Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp
140                145                150

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agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser 155 160 165 170	591
acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser 175 180 185	639
cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg 190 195 200	687
cct gac agt gcc aag gcc tgg ctg tgg atg gat gga acc cct ttc act Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr 205 210 215	735
tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg 220 225 230	783
gac tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys 235 240 245 250	831
gaa ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro 255 260 265	879
gag agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp 270 275 280	921
tgattcgccc tctgcaacta caaatagcag agtgagccag gcggtgccaa agcaagggt	981
agttgagaca ttggaaatg gaacataatc aggaaagact atctctctga ctagtacaaa	1041
atgggttctc gtgtttctct ttcaggatca ccagcatttc tgagcttggg tttatgcacg	1101
tatttaacag tcacaagaag tcttatttcc atgccacca ccaacctcag aaacccataa	1161
tgatcatgac cttcttggtc tagagataac ttttagctct cttctctctc aatgtctaatt	1221
atcacctccc tgttttcatg tcttccttac acctgggtgga ataagaaact ttttgaagta	1281
gaggaaatac attgaggtaa catccttttc tctgacagtc aagtagtcca tcagaaattg	1341
gcagtcactt cccagattgt accagcaaat acacaaggaa ttctttttgt ttgtttcagt	1401
tcatactagt cccctcccaa tccatcagta aagaccccat ctgccttgtc catgcctgtt	1461
cccaacaggg atgtcacttg atatgagaat ctcaaatctc aatgccttat aagcattcct	1521
tcctgtgtcc attaaagctc tgataattgt ctcccccca taggaatttc tcccaggaaa	1581
gaaatataac cccatctccg ttctatatca gaactaccgt ccccgatatt ccttccagag	1641
agattaaaga ccagaaaaaa gtgagcctct tcatctgcac ctgtaaatgt ttcagttcct	1701
attttcttcc attgacctat atttatacct ttcaggtact gaagatttaa taataataaa	1761
tgtaataact gtgaagtgtg tgtgatttca caatggactt atgggttggt ggaaatttca	1821
gcatggaaat gcttttcaaa atatgatagc ggtcattatc ttgattgtgc cttactgaaa	1881

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gtttttgggg aatttacaag agtactgatt acatgattat ctggagaaaa taagatgtct 1941
ttgaaataca tgttggtctc aagaaaacag ttttaacgtt ttcctaaaat gaaatctttt 2001
gagggtgagct tatggcatca acacatgggt gatgaggaag ctgagttgca ttagtgacaca 2061
tgatttccag tcagggtcatg ggaaatgaac agagacagtg acatctttgt agctgctcct 2121
ttgtgaggca cttctttctt gagatgactc catgcacaaa tataacaggg atcattggga 2181
atgacacccat cacagccacc aagnttattg ggttactgat aat 2224

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<210> 23
<211> 280
<212> PRT
<213> Homo sapiens

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<220>
<221> misc_feature
<223> n = a or c or g or t

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<400> 23

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Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
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Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
20 25 30

```

```

Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
35 40 45

```

```

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
50 55 60

```

```

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
65 70 75 80

```

```

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
85 90 95

```

```

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110

```

```

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115 120 125

```

```

Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
130 135 140

```

```

Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
145 150 155 160

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Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
165 170 175

Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe
180 185 190

Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala
195 200 205

Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile
210 215 220

Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
225 230 235 240

Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val
245 250 255

Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro
260 265 270

Pro Glu Thr Leu Gly Glu Gly Asp
275 280

<210> 24
<211> 996
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (38)..(979)

<400> 24
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Met Gln Ala Lys Tyr Ser
1 5

agc acg atg gac atg ctg gat gat gat ggg gac acc acc atg agc ctg 103
Ser Thr Met Asp Met Leu Asp Asp Gly Asp Thr Thr Met Ser Leu
10 15 20

cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc aca 151
His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr
25 30 35

gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc ctg 199
Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr Leu
40 45 50

ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg ctt 247
Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu
55 60 65 70

ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc att 295

<210> 25
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 25

Met Gln Ala Lys Tyr Ser Ser Thr Met Asp Met Leu Asp Asp Gly
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Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
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Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
 35 40 45

Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
 50 55 60

Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
 65 70 75 80

Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
 85 90 95

Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
 100 105 110

Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
 115 120 125

Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu
 130 135 140

Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg
 145 150 155 160

Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr
 165 170 175

Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
 180 185 190

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu
 195 200 205

Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp
 210 215 220

Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp
225 230 235 240

Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr
245 250 255

Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe
260 265 270

Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala
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Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly
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Glu Gly Asp Met His His His His His His
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<210> 26
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<222> (82)..(822)
<223> Xaa = Unknown or other

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ctcaccgctg taggaatcca g atg cag gcc aag tac agc agc acg agg gac 111
Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp
1 5 10
atg ctg gat gat gat ggg gac acc acc atg agc ctg cat tct caa gcc 159
Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala
15 20 25
tct gcc aca act cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac 207
Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr
30 35 40
tac cag ctc tcc aat act ggt caa gac acc att tct caa atg gaa gaa 255
Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu
45 50 55
aga tta gga aat acg tcc caa gag ttg caa tct ctt caa gtc cag aat 303
Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser 60 65 70

ata aag ctt gca gga agt ctg cag cat gtg gct gaa aaa ctc tgt cgt Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg 75 80 85 90	351
gag ctg tat aac aaa gct gga gca cac agg tgc agc cct tgt aca gaa Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu 95 100 105	399
caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac agc Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser 110 115 120	447
aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct ecc Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr 125 130 135	495
atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct cag Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln 140 145 150	543
agc tac tct gag ttt ttc tac tct tat tgg aca ggc ctt ttg cgc cct Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro 155 160 165	591
gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act tct Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser 175 180 185	639
gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga gac Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp 190 195 200	687
tgt gtg gcc atc ctt aat ggg atg atc ttc tca aag gac tgc aaa gaa Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu 205 210 215	735
ttg aag cgt tgt gtc tgt gag aga agg gca gga atg gtg aag cca gag Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu 220 225 230	783
agc ctc cat gtc ccc cct gaa aca tta ggc gaa ggt gac tgattgcgcc Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu Gly Asp 235 240 245	832
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gtgtttccctg ttcaggatca ccagcatttc tgagcttggg tttatgcacg tatttaacag	1012
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 cccatctcgc ttctatatca gaactaccgt ccccgatatt ccttcagag agattaaaga 1552
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 aatttacaag agtactgatt acatgattat ctggagaaaa taagatgtct ctgaaataca 1852
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 tcagggtcat ggaaatgaac agagacagtg acatctttgt agctgtctct ttgtgaggca 2032
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 <212> PRT
 <213> Homo sapiens
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Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Gly
 1 5 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
 20 25 30

Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr
 35 40 45

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser
 50 55 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser
 65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala
 85 90 95

Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly
 100 105 110

Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys
115 120 125

Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys
130 135 140

Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe
145 150 155 160

Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp
165 170 175

Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
180 185 190

Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn
195 200 205

Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys
210 215 220

Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro
225 230 235 240

Glu Thr Leu Gly Glu Gly Asp
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<210> 28
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<212> DNA
<213> Homo sapiens

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<222> (199)..(2457)

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aagtctctagg actgatctcc agggaccagca ctcttctccc agcccttagg gtctgtgctg 180
gccaaaggcct tccctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc 231
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro 1 5 10
tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tgc tgc ttg ggg tct ccg 279
Trp Gly Leu Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro 15 20 25
tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg 327
Ser Pro Ser Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg 30 35 40

ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag Phe Arg Leu Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu 45 50 55	375
ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg Ile Gln Arg Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr 60 65 70 75	423
ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag gcc Leu Gln Ala Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala 80 85 90	471
aca ggc tgg acc cac agt gcc aag tat ggc cct gga aca ggc cgc atc Thr Gly Trp Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile 95 100 105	519
tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa Trp Leu Asp Asn Leu Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu 110 115 120	567
tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag gat Cys Ala Ser Arg Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp 125 130 135	615
gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tgc gac tcc Ala Gly Val Ile Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser 140 145 150 155	663
aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga att Asn Val Ile Glu Val Glu His His Leu Gln Val Glu Val Arg Ile 160 165 170	711
cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag ggg Arg Pro Ala Val Gly Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly 175 180 185	759
ctg gtg gaa gtc agg ctt cct gac ggc tgg tgc caa gtg tgc gac aaa Leu Val Glu Val Arg Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys 190 195 200	807
ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc ttc Gly Trp Ser Ala His Asn Ser His Val Val Cys Gly Met Leu Gly Phe 205 210 215	855
ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc caa Pro Ser Glu Lys Arg Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln 220 225 230 235	903
cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg Arg Gln Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr 240 245 250	951
gag gcc cac ctc tcc ctc tgt tcc ctg gag ttc tat cgt gcc aat gac Glu Ala His Leu Ser Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp 255 260 265	999
acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg cca Thr Ala Arg Cys Pro Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro 270 275 280	1047
ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag tgc Gly Pro Val Tyr Ala Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser 285 290 295	1095

aag cct cag ggg gag gtc cgt gtc cgt cta aag ggc ggc gcc cac cct Lys Pro Gln Gly Glu Val Arg Val Arg Leu Lys Gly Gly Ala His Pro 300 305 310 315	1143
gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca gtc Gly Glu Gly Arg Val Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val 320 325 330	1191
tgt tac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg gag Cys Tyr Arg Lys Trp Asp Leu His Ala Ala Ser Val Val Cys Arg Glu 335 340 345	1239
ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg ggg Leu Gly Phe Gly Ser Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly 350 355 360	1287
cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tct gga cag Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln 365 370 375	1335
gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag gat Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp 380 385 390 395	1383
tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac act Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr 400 405 410	1431
ggg gca gag acc agg atc cga ctc agt ggg ggc cgc agc caa cat gag Gly Ala Glu Thr Arg Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu 415 420 425	1479
ggg cga gtc gag gtg caa ata ggg gga cct ggg ccc ctt cgc tgg ggc Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly 430 435 440	1527
ctc atc tgt ggg gat gac tgg ggg acc ctg gag gcc atg gtg gcc tgt Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys 445 450 455	1575
agg caa ctg ggt ctg ggc tac gcc aac cac ggc ctg cag gag acc tgg Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp 460 465 470 475	1623
tac tgg gac tct ggg aat ata aca gag gtg gtg atg agt gga gtg cgc Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser Gly Val Arg 480 485 490	1671
tgc aca ggg act gag ctg tcc ctg gat cag tgt gcc cat cat ggc acc Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His His Gly Thr 495 500 505	1719
cac atc acc tgc aag agg aca ggg acc cgc ttc act gct gga gtc atc His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile 510 515 520	1767
tgt tct gag act gca tca gat ctg ttg ctg cac tca gca ctg gtg cag Cys Ser Glu Thr Ala Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln 525 530 535	1815
gag acc gcc tac atc gaa gac cgg ccc ctg cat atg ttg tac tgt gct Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala 540 545 550 555	1863

gcg gaa gag aac tgc ctg gcc agc tca gcc cgc tca gcc aac tgg ccc Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro 560 565 570	1911
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gga cga gct gac ttc agg ccc aag gct ggg cgc cac tcc tgg gtg tgg Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp 590 595 600	2007
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gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa gct Asp Ile Leu Thr Pro Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala 620 625 630 635	2103
agt ttc tgt ctc gaa gac act gag tgt cag gag gat gtc tcc aag cgg Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg 640 645 650	2151
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gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac tgc Glu Val Ala Glu Ser Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys 700 705 710 715	2343
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gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc cag Ala Phe Ser Glu Glu Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln 735 740 745	2439
acc agc aac cag att atc taagtgccac tggcctctgc aaaccaccac Thr Ser Asn Gln Ile Ile 750	2487
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cgctcagga	cttcgggtcc	cctcaccctg	ggcggtatgc	caaagactcc	gccttcccaa	4767

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<210> 29
 <211> 753
 <212> PRT
 <213> Homo sapiens

<400> 29

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
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Cys Leu Leu Cys Ser Ser Cys-Leu Gly Ser Pro Ser Pro Ser Thr Gly
 20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
 35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
 50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
 65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
 85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
 100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
 115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
 130 135 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
 145 150 155 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
 165 170 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg

180

185

190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
210 215 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225 230 235 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
245 250 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
260 265 270

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
290 295 300

Val Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Tyr Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Ile Arg Leu Ser Gly Gly Arg Ser Glu His Glu Gly Arg Val Glu Val
420 425 430

Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp
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Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu
450 455 460

Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly
465 470 475 480

Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu
485 490 495

Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys
500 505 510

Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala
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Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile
530 535 540

Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys
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Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg
565 570 575

Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe
580 585 590

Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly
595 600 605

His Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro
610 615 620

Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu
625 630 635 640

Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn
645 650 655

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His
660 665 670

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn
675 680 685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser
690 695 700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His
705 710 715 720

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu
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cctgcc atg cga cct gtc agt gtc tgg cag tgg agc ccc tgg ggg ctg 168
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu
1 5 10
ctg ctg tgc ctg ctg tgc agt tgc tgc ttg ggg tct cca tcc cct tcc 216
Leu Leu Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser
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acg ggc cct gag aag aag gcc ggg agc cag ggg ctt cgg ttc cgg ctg 264
Thr Gly Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu
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gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg gag ata cag cga 312
Ala Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg
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gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc acg ctg cag gct 360
Ala Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala
65 70 75
gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag gcc aca ggc tgg 408
Ala His Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp
80 85 90
acc cac agt gcc aaa tat ggc cct gga aca ggc cgc atc tgg ctg gac 456
Thr His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp
95 100 105 110
aac ttg agc tgc agt ggg acc gag cag agt gtg act gaa tgt gcc tcc 504

Asn	Leu	Ser	Cys	Ser	Gly	Thr	Glu	Gln	Ser	Val	Thr	Glu	Cys	Ala	Ser		
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cgg	ggc	tgg	ggg	aac	agt	gac	tgt	acg	cac	gat	gag	gat	gct	ggg	gtc	552	
Arg	Gly	Trp	Gly	Asn	Ser	Asp	Cys	Thr	His	Asp	Glu	Asp	Ala	Gly	Val		
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atc	tgc	aaa	gac	cag	cgc	ctc	cct	ggc	ttc	tcg	gac	tcc	aat	gtc	att	600	
Ile	Cys	Lys	Asp	Gln	Arg	Leu	Pro	Gly	Phe	Ser	Asp	Ser	Asn	Val	Ile		
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gag	gcc	cgt	gtc	cgt	cta	aag	ggc	ggc	gcc	cac	cct	gga	gag	ggc	cgg	648	
Glu	Ala	Arg	Val	Arg	Leu	Lys	Gly	Gly	Ala	His	Pro	Gly	Glu	Gly	Arg		
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Val	Glu	Val	Leu	Lys	Ala	Ser	Thr	Trp	Gly	Val	Val	Cys	Asp	Arg	Lys		
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tgg	gac	ctg	cat	gca	gcc	agc	gtg	gtg	tgt	cgg	gag	ctg	ggc	ttc	ggg	744	
Trp	Asp	Leu	His	Ala	Ala	Ser	Val	Val	Cys	Arg	Glu	Leu	Gly	Phe	Gly		
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Ser	Ala	Arg	Glu	Ala	Leu	Ser	Gly	Ala	Arg	Met	Gly	Gln	Gly	Met	Gly		
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gct	atc	cac	ctg	agt	gaa	gtt	cgc	tgc	tct	gga	cag	gag	ctc	tcc	ctc	840	
Ala	Ile	His	Leu	Ser	Glu	Val	Arg	Cys	Ser	Gly	Gln	Glu	Leu	Ser	Leu		
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tgg	aag	tgc	ccc	cac	aag	aac	atc	aca	gct	gag	gat	tgt	tca	cat	agc	888	
Trp	Lys	Cys	Pro	His	Lys	Asn	Ile	Thr	Ala	Glu	Asp	Cys	Ser	His	Ser		
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cag	gat	gcc	ggg	gtc	cgg	tgc	aac	cta	cct	tac	act	ggg	gca	gag	acc	936	
Gln	Asp	Ala	Gly	Val	Arg	Cys	Asn	Leu	Pro	Tyr	Thr	Gly	Ala	Glu	Thr		
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agg	atc	cga	ctc	agt	ggg	ggc	cgc	agc	caa	cat	gag	ggg	cga	gtc	gag	984	
Arg	Ile	Arg	Leu	Ser	Gly	Gly	Arg	Ser	Gln	His	Glu	Gly	Arg	Val	Glu		
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gtg	caa	ata	ggg	gga	cct	ggg	ccc	ctt	cgc	tgg	ggc	ctc	atc	tgt	ggg	1032	
Val	Gln	Ile	Gly	Gly	Pro	Gly	Pro	Leu	Arg	Trp	Gly	Leu	Ile	Cys	Gly		
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ctg	ggc	tac	gcc	aac	cac	ggc	ctg	cag	gag	acc	tgg	tac	tgg	gac	tct	1128	
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Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
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Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys

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Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln Asp 245 250 255		
Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg Ile 260 265 270		
Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val Gln 275 280 285		
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Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu Gly 305 310 315 320		
Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn 325 330 335		
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Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys Arg 355 360 365		
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Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu
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Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu
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Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg Leu
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Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe Arg
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Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly His
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Tyr His Ser Met Asp Phe Phe Thr His Tyr Asp Ile Leu Thr Pro Asn
465 470 475 480

Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp
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Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn Phe
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Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His Asp
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Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser Asp
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Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His Arg
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Gly Asp Pro Asp Cys Pro Asp Asp Ser Asp Glu Ser Leu Asp Thr Cys	
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Pro Glu Glu Val Glu Ile Lys Cys Pro Leu Asn His Ile Ala Cys Leu	
110 115 120	

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att ctt caa tcc ttc cac aat gtg caa caa atg gcg att gac tgg ctc Ile Leu Gln Ser Phe His Asn Val Gln Gln Met Ala Ile Asp Trp Leu 315 320 325 330	1851
act cga aat ctc tat ttt gtg gac cat gtc ggt gac cgg atc ttt gtt Thr Arg Asn Leu Tyr Phe Val Asp His Val Gly Asp Arg Ile Phe Val 335 340 345	1899
tgt aat tcc aac ggt tct gta tgt gtc acc ctg att gat ctg gag ctt Cys Asn Ser Asn Gly Ser Val Cys Val Thr Leu Ile Asp Leu Glu Leu 350 355 360	1947
cac aat cct aaa gca ata gca gta gat cca ata gca gga aaa ctt ttc His Asn Pro Lys Ala Ile Ala Val Asp Pro Ile Ala Gly Lys Leu Phe 365 370 375	1995

ttt act gac tac ggg aat gtc gcc aaa gtg gag aga tgt gac atg gat Phe Thr Asp Tyr Gly Asn Val Ala Lys Val Glu Arg Cys Asp Met Asp 380 385 390	2043
ggg atg aac cga aca agg ata att gat tca aag aca gag cag cca gct Gly Met Asn Arg Thr Arg Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala 395 400 410	2091
gca ctg gca cta gac cta gtc aac aaa ttg gtt tac tgg gta gat ctt Ala Leu Ala Leu Asp Leu Val Asn Lys Leu Val Tyr Trp Val Asp Leu 415 420 425	2139
tac ttg gac tat gtg gga gta gtg gac tat caa gga aaa aat aga cac Tyr Leu Asp Tyr Val Gly Val Val Asp Tyr Gln Gly Lys Asn Arg His 430 435 440	2187
act gtc att caa ggc aga caa gtc aga cat ctt tat ggt ata act gtg Thr Val Ile Gln Gly Arg Gln Val Arg His Leu Tyr Gly Ile Thr Val 445 450 455	2235
ttt gaa gat tat ttg tat gca acc aat tct gat aac tac aat atc gta Phe Glu Asp Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val 460 465 470	2283
agg ata aac cga ttt aat ggg act gat att cac tca tta att aaa att Arg Ile Asn Arg Phe Asn Gly Thr Asp Ile His Ser Leu Ile Lys Ile 475 480 485 490	2331
gag aat gct tgg gga atc cga att tat caa aaa aga act caa cca aca Glu Asn Ala Trp Gly Ile Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr 495 500 505	2379
gtc aga agc cat gca tgt gaa gtc gat cca tat gga atg cca ggg ggc Val Arg Ser His Ala Cys Glu Val Asp Pro Tyr Gly Met Pro Gly Gly 510 515 520	2427
tgt tca cac atc tgt cta ctc agc agc agt tac aaa act cgg act tgt Cys Ser His Ile Cys Leu Leu Ser Ser Tyr Lys Thr Arg Thr Cys 525 530 535	2475
cgc tgc agg act ggc ttc aac ttg gga agt gat ggc agg tca tgc aaa Arg Cys Arg Thr Gly Phe Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys 540 545 550	2523
aga cca aag aat gag ttg ttc ctc ttt tat ggg aaa gga cgc cca gga Arg Pro Lys Asn Glu Leu Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly 555 560 565 570	2571
att gtt aga gga atg gac ttg aat acc aag ata gct gat gaa tac atg Ile Val Arg Gly Met Asp Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met 575 580 585	2619
atc ccc ata gaa aat ctg gta aac cct cgt gct tta gac ttt cac gca Ile Pro Ile Glu Asn Leu Val Asn Pro Arg Ala Leu Asp Phe His Ala 590 595 600	2667
gaa acc aat tac atc tac ttt gct gac acc acc agt ttc cta att ggc Glu Thr Asn Tyr Ile Tyr Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly 605 610 615	2715
cgg cag aag ata gat ggc aca gag aga gaa acc atc ctg aaa gat gat Arg Gln Lys Ile Asp Gly Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp 620 625 630	2763

ctg gat aat gta gag ggc att gct gtg gac tgg att gga aat aat ctt Leu Asp Asn Val Glu Gly Ile Ala Val Asp Trp Ile Gly Asn Asn Leu 635 640 645 650	2811
tac tgg acc aat gat ggc cat agg aaa acc att aat gtg gct agg ctg Tyr Trp Thr Asn Asp Gly His Arg Lys Thr Ile Asn Val Ala Arg Leu 655 660 665	2859
gaa aaa gct tct cag agt cgg aag act ctt tta gag ggt gaa atg tct Glu Lys Ala Ser Gln Ser Arg Lys Thr Leu Leu Glu Gly Glu Met Ser 670 675 680	2907
cat ccc aga gga att gtg gtg gat cca att aat ggt tgg atg tat tgg His Pro Arg Gly Ile Val Val Asp Pro Ile Asn Gly Trp Met Tyr Trp 685 690 695	2955
aca gac tgg gag gaa gat gaa ata gat gac agc gtg gga agg att gag Thr Asp Trp Glu Glu Asp Glu Ile Asp Asp Ser Val Gly Arg Ile Glu 700 705 710	3003
aag gcc tgg atg gat gga ttc aat cgg cag att ttt gtg act tca aag Lys Ala Trp Met Asp Gly Phe Asn Arg Gln Ile Phe Val Thr Ser Lys 715 720 725 730	3051
atg ctg tgg cca aac ggt tta act ctg gac ttt cac acc aac aca tta Met Leu Trp Pro Asn Gly Leu Thr Leu Asp Phe His Thr Asn Thr Leu 735 740 745	3099
tac tgg tgt gat gcc tat tac gat cat att gaa aaa gta ttt ttg aat Tyr Trp Cys Asp Ala Tyr Tyr Asp His Ile Glu Lys Val Phe Leu Asn 750 755 760	3147
ggg act cac agg aag att gtt tac agt ggg aga gag ttg aac cac cct Gly Thr His Arg Lys Ile Val Tyr Ser Gly Arg Glu Leu Asn His Pro 765 770 775	3195
ttc gga ctg tcg cat cat gga aat tat gtg ttc tgg act gat tat atg Phe Gly Leu Ser His His Gly Asn Tyr Val Phe Trp Thr Asp Tyr Met 780 785 790	3243
aat ggt tcc att ttt caa cta gat ttg ata aca agt gag gtg aca ttg Asn Gly Ser Ile Phe Gln Leu Asp Leu Ile Thr Ser Glu Val Thr Leu 795 800 805 810	3291
ctg agg cat gaa aga cca ccc cta ttt ggg ctt cag att tat gat cca Leu Arg His Glu Arg Pro Pro Leu Phe Gly Leu Gln Ile Tyr Asp Pro 815 820 825	3339
cga aag caa caa ggt gac aat atg tgc cga gta aat aat ggg ggc tgt Arg Lys Gln Gln Gly Asp Asn Met Cys Arg Val Asn Asn Gly Gly Cys 830 835 840	3387
agt aca ctt tgc ttg gct atc cca gga ggc cgg gtg tgt gct tgt gcc Ser Thr Leu Cys Leu Ala Ile Pro Gly Gly Arg Val Cys Ala Cys Ala 845 850 855	3435
gat aat caa ctt ttg gat gaa aat ggg aca act tgc aca ttt aat cct Asp Asn Gln Leu Leu Asp Glu Asn Gly Thr Thr Cys Thr Phe Asn Pro 860 865 870	3483
gga gaa gca cta cct cac ata tgt aaa gct gga gag ttt cgc tgc aaa Gly Glu Ala Leu Pro His Ile Cys Lys Ala Gly Glu Phe Arg Cys Lys 875 880 885 890	3531

aac aga cac tgt atc caa gct cgg tgg aaa tgt gat ggc gac gat gac Asn Arg His Cys Ile Gln Ala Arg Trp Lys Cys Asp Gly Asp Asp 895 900 905	3579
tgc cta gac gga agc gat gag gat tca gta aac tgc ttc aat cat agc Cys Leu Asp Gly Ser Asp Glu Asp Ser Val Asn Cys Phe Asn His Ser 910 915 920	3627
tgt cct gat gat cag ttt aaa tgc cag aat aat cgc tgc atc ccc aag Cys Pro Asp Asp Gln Phe Lys Cys Gln Asn Asn Arg Cys Ile Pro Lys 925 930 935	3675
aga tgg ctt tgt gat gga gct aat gac tgt ggg agc aat gaa gat gaa Arg Trp Leu Cys Asp Gly Ala Asn Asp Cys Gly Ser Asn Glu Asp Glu 940 945 950	3723
tcc aat caa act tgc aca gcc aga aca tgc cag gta gac cag ttt tct Ser Asn Gln Thr Cys Thr Ala Arg Thr Cys Gln Val Asp Gln Phe Ser 955 960 965 970	3771
tgc gga aat ggg cgt tgc att ccc aga gca tgg ctg tgt gac agg gaa Cys Gly Asn Gly Arg Cys Ile Pro Arg Ala Trp Leu Cys Asp Arg Glu 975 980 985	3819
gac gac tgt ggt gac cag aca gat gaa atg gca tct tgt gaa ttc cca Asp Asp Cys Gly Asp Gln Thr Asp Glu Met Ala Ser Cys Glu Phe Pro 990 995 1000	3867
act tgt gag cca cta acc caa ttc gta tgc aaa agt gga aga tgc Thr Cys Glu Pro Leu Thr Gln Phe Val Cys Lys Ser Gly Arg Cys 1005 1010 1015	3912
att agc agc aaa tgg cac tgc gac tct gat gac gac tgt ggg gac Ile Ser Ser Lys Trp His Cys Asp Ser Asp Asp Asp Cys Gly Asp 1020 1025 1030	3957
ggg agt gat gag gtg ggc tgt gtt cac tct tgc ttt gat aat cag Gly Ser Asp Glu Val Gly Cys Val His Ser Cys Phe Asp Asn Gln 1035 1040 1045	4002
ttc aga tgt tcc agt ggc aga tgc atc sca ggc cac tgg gcc tgt Phe Arg Cys Ser Ser Gly Arg Cys Ile Pro Gly His Trp Ala Cys 1050 1055 1060	4047
gat ggt gac aat gac tgt ggg gac ttc agt gat gaa gcc cag atc Asp Gly Asp Asn Asp Cys Gly Asp Phe Ser Asp Glu Ala Gln Ile 1065 1070 1075	4092
aat tgt act aaa gaa gag att cat tct cct gct ggt tgt aac gga Asn Cys Thr Lys Glu Glu Ile His Ser Pro Ala Gly Cys Asn Gly 1080 1085 1090	4137
aat gaa ttt cag tgc cac cct gat ggt aat tgc gtt cct gat ttg Asn Glu Phe Gln Cys His Pro Asp Gly Asn Cys Val Pro Asp Leu 1095 1100 1105	4182
tgg cgc tgt gat gga gaa aaa gac tgt gaa gat ggt agt gat gaa Trp Arg Cys Asp Gly Glu Lys Asp Cys Glu Asp Gly Ser Asp Glu 1110 1115 1120	4227
aaa ggt tgc aat ggt acc ata cga ttg tgt gac cac aaa acc aag Lys Gly Cys Asn Gly Thr Ile Arg Leu Cys Asp His Lys Thr Lys 1125 1130 1135	4272

ttt tcc tgt	tgg agt aca ggg aga	tgc atc aac aaa gca	tgg gtg	4317
Phe Ser Cys	Trp Ser Thr Gly Arg	Cys Ile Asn Lys Ala	Trp Val	
1140	1145	1150		
tgt gat gga	gat att gat tgc gaa	gat cag tca gat gaa	gat gac	4362
Cys Asp Gly	Asp Ile Asp Cys Glu	Asp Gln Ser Asp Glu	Asp Asp	
1155	1160	1165		
tgt gac agt	ttc ttg tgt gga cca	ccc aag cat cct tgt	gct aat	4407
Cys Asp Ser	Phe Leu Cys Gly Pro	Pro Lys His Pro Cys	Ala Asn	
1170	1175	1180		
gac acc tca	gcc tgc ctg cag cca	gag aaa ctg tgc aat	ggg aaa	4452
Asp Thr Ser	Val Cys Leu Gln Pro	Glu Lys Leu Cys Asn	Gly Lys	
1185	1190	1195		
aag gat tgt	cct gat ggc tct gat	gaa ggc tat ctg tgt	gat gag	4497
Lys Asp Cys	Pro Asp Gly Ser Asp	Glu Gly Tyr Leu Cys	Asp Glu	
1200	1205	1210		
tgt tgc ctg	aac aat gga ggc tgt	agc aac cac tgt tct	gtt gtt	4542
Cys Ser Leu	Asn Asn Gly Gly Cys	Ser Asn His Cys Ser	Val Val	
1215	1220	1225		
cct gga aga	gga att gtc tgt tcc	tgc cct gaa gga ctt	caa ctg	4587
Pro Gly Arg	Gly Ile Val Cys Cys	Cys Pro Glu Gly Leu	Gln Leu	
1230	1235	1240		
aac aaa gac	aat aaa aca tgt gaa	att gtg gat tat tgt	agc aat	4632
Asn Lys Asp	Asn Lys Thr Cys Glu	Ile Val Asp Tyr Cys	Ser Asn	
1245	1250	1255		
cat cta aag	tgc agc caa gta tgt	gag cag cac aag cac	aca gtc	4677
His Leu Lys	Cys Ser Gln Val Cys	Glu Gln His Lys His	Thr Val	
1260	1265	1270		
aag tgc tca	tgt tat gaa ggt tgg	aug ctg gat gta gac	ggt gaa	4722
Lys Cys Ser	Cys Tyr Glu Gly Trp	Lys Leu Asp Val Asp	Gly Glu	
1275	1280	1285		
agt tgt aca	agt gtt gat cct ttt	gaa gca ttc atc atc	ttt tct	4767
Ser Cys Thr	Ser Val Asp Pro Phe	Glu Ala Phe Ile Ile	Phe Ser	
1290	1295	1300		
att cgt cat	gag atc aga agg att	gat ctt cac aaa aga	gac tat	4812
Ile Arg His	Glu Ile Arg Arg Ile	Asp Leu His Lys Arg	Asp Tyr	
1305	1310	1315		
agt cta ctt	gtt cct gga ttg aga	aac aca ata gca ctt	gat ttt	4857
Ser Leu Leu	Val Pro Gly Leu Arg	Asn Thr Ile Ala Leu	Asp Phe	
1320	1325	1330		
cac ttc aat	caa agt tta ctt tat	tgg aca gat gtt gta	gaa gac	4902
His Phe Asn	Gln Ser Leu Leu Tyr	Trp Thr Asp Val Val	Glu Asp	
1335	1340	1345		
aga ata tac	cgg gga aag ctt tct	gaa agt gga ggt gtc	agt gcc	4947
Arg Ile Tyr	Arg Gly Lys Leu Ser	Glu Ser Gly Gly Val	Ser Ala	
1350	1355	1360		
att gaa gtg	gtt gtg gag cat ggc	ctg gct act cca gaa	ggc ctg	4992
Ile Glu Val	Val Val Glu His Gly	Leu Ala Thr Pro Glu	Gly Leu	
1365	1370	1375		

aca gtc gac	tgg ata gca gga aac	ata tac tgg ata gac	agc aat	5037
Thr Val Asp	Trp Ile Ala Gly Asn	Ile Tyr Trp Ile Asp	Ser Asn	
1380	1385	1390		
ctg gac caa	atc gaa gtg gcc aaa	cta gat ggc tcc cta	aga act	5082
Leu Asp Gln	Ile Glu Val Ala Lys	Leu Asp Gly Ser Leu	Arg Thr	
1395	1400	1405		
aca cta ata	gca gga gcc atg gaa	cac ccc agg gcc att	gct ttg	5127
Thr Leu Ile	Ala Gly Ala Met Glu	His Pro Arg Ala Ile	Ala Leu	
1410	1415	1420		
gac cca aga	tat gga att ctt ttc	tgg aca gac tgg gat	gca aat	5172
Asp Pro Arg	Tyr Gly Ile Leu Phe	Trp Thr Asp Trp Asp	Ala Asn	
1425	1430	1435		
ttt cot cgc	att gaa tct gcc tct	atg agt ggt gct ggg	aga aaa	5217
Phe Pro Arg	Ile Glu Ser Ala Ser	Met Ser Gly Ala Gly	Arg Lys	
1440	1445	1450		
acc atc tat	aaa gac atg aaa act	ggg gct tgg cct aat	gga cta	5262
Thr Ile Tyr	Lys Asp Met Lys Thr	Gly Ala Trp Pro Asn	Gly Leu	
1455	1460	1465		
act gtg gac	cac ttt gag aaa agg	ata gtg tgg aca gac	gcc agg	5307
Thr Val Asp	His Phe Glu Lys Arg	Ile Val Trp Thr Asp	Ala Arg	
1470	1475	1480		
tca gat gct	att tat tca gcc ctc	tat gat gga aca aac	atg ata	5352
Ser Asp Ala	Ile Tyr Ser Ala Leu	Tyr Asp Gly Thr Asn	Met Ile	
1485	1490	1495		
gaa atc atc	cga ggt cat gaa tac	ctt tcc cat ccc ttt	gct gtg	5397
Glu Ile Ile	Arg Gly His Glu Tyr	Leu Ser His Pro Phe	Ala Val	
1500	1505	1510		
tct cta tat	ggg agt gaa gtc tac	tgg aca gac tgg agg	acc aac	5442
Ser Leu Tyr	Gly Ser Glu Val Tyr	Trp Thr Asp Trp Arg	Thr Asn	
1515	1520	1525		
aca ttg tcc	aaa gcc aat aag tgg	aca ggg cag aat gtc	agt gtg	5487
Thr Leu Ser	Lys Ala Asn Lys Trp	Thr Gly Gln Asn Val	Ser Val	
1530	1535	1540		
att cag aaa	acc agt gca cag cca	ttt gac ctt cag ata	tac cat	5532
Ile Gln Lys	Thr Ser Ala Gln Pro	Phe Asp Leu Gln Ile	Tyr His	
1545	1550	1555		
ccc agt cgc	cag cca cag gct ccc	aat cct tgt gca gct	aat gat	5577
Pro Ser Arg	Gln Pro Gln Ala Pro	Asn Pro Cys Ala Ala	Asn Asp	
1560	1565	1570		
ggc aaa ggc	ccc tgc tct cac atg	tgt cta atc aat cac	aat agg	5622
Gly Lys Gly	Pro Cys Ser His Met	Cys Leu Ile Asn His	Asn Arg	
1575	1580	1585		
agt gct gcc	tgt gcg tgc ccc cac	ttg atg aag ctt tct	tca gac	5667
Ser Ala Ala	Cys Ala Cys Pro His	Leu Met Lys Leu Ser	Ser Asp	
1590	1595	1600		
aag aag acc	tgc tat gaa atg aaa	aaa ttt ctt ctt tat	gca aga	5712
Lys Lys Thr	Cys Tyr Glu Met Lys	Lys Phe Leu Leu Tyr	Ala Arg	
1605	1610	1615		

cgt tct gaa atc aga gga gtg gat att gac aat cca tac ttt aac Arg Ser Glu Ile Arg Gly Val Asp Ile Asp Asn Pro Tyr Phe Asn 1620 1625 1630	5757
ttc atc acg gca ttt aca gtc cct gat att gat gac gtt act gtg Phe Ile Thr Ala Phe Thr Val Pro Asp Ile Asp Asp Val Thr Val 1635 1640 1645	5802
ata gac ttc gat gca tct gag gaa cgt tta tac tgg aca gat att Ile Asp Phe Asp Ala Ser Glu Glu Pro Arg Leu Tyr Trp Thr Asp Ile 1650 1655 1660	5847
aaa aca caa acc att aaa cga gct ttt att aac gga act ggg tta Lys Thr Gln Thr Ile Lys Arg Ala Phe Ile Asn Gly Thr Gly Leu 1665 1670 1675	5892
gaa act gtt att tca aga gat atr cag agt atc aga ggg cta gca Glu Thr Val Ile Ser Arg Asp Ile Gln Ser Ile Arg Gly Leu Ala 1680 1685 1690	5937
gtg gat tgg gtg tca cgt aat tta tac tgg att agc tca gaa ttt Val Asp Trp Val Ser Arg Asn Leu Tyr Trp Ile Ser Ser Glu Phe 1695 1700 1705	5982
gat gaa acg caa att aat gtg gca agg cta gat ggc tot ttg aaa Asp Glu Thr Gln Ile Asn Val Ala Arg Leu Asp Gly Ser Leu Lys 1710 1715 1720	6027
acc tca att atc cat gga atc gat aag cca cag tgt ctt gca gct Thr Ser Ile Ile His Gly Ile Asp Lys Pro Gln Cys Leu Ala Ala 1725 1730 1735	6072
cac cca gtc agg gga aaa ctc tac tgg acc gat gga aac aca att His Pro Val Arg Gly Lys Leu Tyr Trp Thr Asp Gly Asn Thr Ile 1740 1745 1750	6117
aac atg gca aat atg gat ggc agt aat agc aag att ctg ttt cag Asn Met Ala Asn Met Asp Gly Ser Asn Ser Lys Ile Leu Phe Gln 1755 1760 1765	6162
aat cag aag gag cca gtt ggt cta tgc ata gac tat gtg gaa aac Asn Gln Lys Glu Pro Val Gly Leu Ser Ile Asp Tyr Val Glu Asn 1770 1775 1780	6207
aag ctt tat tgg atc agt tgc ggg aat gga acc ata aat aga tgc Lys Leu Tyr Trp Ile Ser Ser Gly Asn Gly Thr Ile Asn Arg Cys 1785 1790 1795	6252
aac ctg gat ggt ggt aat tca gaa gta atc gag tca atg aaa gaa Asn Leu Asp Gly Gly Asn Leu Glu Val Ile Glu Ser Met Lys Glu 1800 1805 1810	6297
gaa tta aca aaa gct aca gcc cta acc atc atg gat aag aaa ctg Glu Leu Thr Lys Ala Thr Ala Leu Thr Ile Met Asp Lys Lys Leu 1815 1820 1825	6342
tgg tgg gca gac caa aac tta gcc cag cta gga acc tgc agc aaa Trp Trp Ala Asp Gln Asn Leu Ala Gln Leu Gly Thr Cys Ser Lys 1830 1835 1840	6387
aga gac gga aga aac ccc acc atc cta cgg aat aag act tot ggg Arg Asp Gly Arg Asn Pro Thr Ile Leu Arg Asn Lys Thr Ser Gly 1845 1850 1855	6432

gta gtt cat	atg aaa gtc	tat gat	aaa gaa gca	cag caa	ggc agc	6477
Val Val His	Met Lys Val Tyr	Asp	Lys Glu Ala Gln	Gln	Gly Ser	
1860		1865		1870		
aat tcc tgc	caa cta aac	aat ggt	gga tgc tct	caa ctt	tgt tta	6522
Asn Ser Cys	Gln Leu Asn Asn	Gly	Gly Cys Ser Gln	Leu	Cys Leu	
1875		1880		1885		
cca aca tct	gaa act aca	agg act	tgt atg tgt	aca gtg	gga tat	6567
Pro Thr Ser	Glu Thr Thr Arg	Thr	Cys Met Cys Thr	Val	Gly Tyr	
1890		1895		1900		
tat ctc caa	aag aac cgt	atg tca	tgt caa ggt	ata gaa	tca ttt	6612
Tyr Leu Gln	Lys Asn Arg Met	Ser	Cys Gln Gly Ile	Glu	Ser Phe	
1905		1910		1915		
ctt atg tac	tct gtt cat	gaa gga	atc agg gga	ata cct	ctt gaa	6657
Leu Met Tyr	Ser Val His Glu	Gly	Ile Arg Gly Ile	Pro	Leu Glu	
1920		1925		1930		
cca agt gac	aaa atg gat	gct ttg	atg cct ata	tca gga	act tca	6702
Pro Ser Asp	Lys Met Asp Ala	Leu	Met Pro Ile Ser	Gly	Thr Ser	
1935		1940		1945		
ttt gcc tgg	gga ata gat	ttc cat	gca gaa aat	gat acc	atc tac	6747
Phe Ala Val	Gly Ile Asp Phe	His	Ala Glu Asn Asp	Thr	Ile Tyr	
1950		1955		1960		
tgg aca gac	atg ggc ttc	aat aaa	att agc aga	gct aaa	aga gat	6792
Trp Thr Asp	Met Gly Phe Asn	Lys	Ile Ser Arg Ala	Lys	Arg Asp	
1965		1970		1975		
cag act tgg	aaa gaa gat	atc att	acc aat ggc	ttg gga	aga gtg	6837
Gln Thr Trp	Lys Glu Asp Ile	Ile	Thr Asn Gly Leu	Gly	Arg Val	
1980		1985		1990		
gaa ggg ata	gct gtt gac	tgg att	gct ggt aac	ata tat	tgg aca	6882
Glu Gly Ile	Ala Val Asp Trp	Ile	Ala Gly Asn Ile	Tyr	Trp Thr	
1995		2000		2005		
gat cat ggt	ttc aac tta	att gaa	gtt gca aga	ctc aat	ggt tct	6927
Asp His Gly	Phe Asn Leu Ile	Glu	Val Ala Arg Leu	Asn	Gly Ser	
2010		2015		2020		
ttc cgt tat	gta att att	tcc caa	ggc ctg gat	caa cca	aga tct	6972
Phe Arg Tyr	Val Ile Ile Ser	Gln	Gly Leu Asp Gln	Pro	Arg Ser	
2025		2030		2035		
ata gct tgg	cac cca gag	aaa ggc	ctc ttg ttc	tgg act	gaa tgg	7017
Ile Ala Val	His Pro Glu Lys	Gly	Leu Leu Phe Trp	Thr	Glu Trp	
2040		2045		2050		
gga caa atg	ccc tgt att	gga aag	gct cgc ttg	gat ggc	tca gag	7062
Gly Gln Met	Pro Cys Ile Gly	Lys	Ala Arg Leu Asp	Gly	Ser Glu	
2055		2060		2065		
aag gtt gtc	ctt gta agc	atg gga	ata gca tgg	ccg aat	ggc atc	7107
Lys Val Val	Leu Val Ser Met	Gly	Ile Ala Trp Pro	Asn	Gly Ile	
2070		2075		2080		
tcc atc gac	tat gag gaa	aat aaa	ttg tac tgg	tgt gat	gct cgc	7152
Ser Ile Asp	Tyr Glu Glu Asn	Lys	Leu Tyr Trp Cys	Asp	Ala Arg	
2085		2090		2095		

aca gac aag Thr Asp Lys 2100	ata gag aga atc Ile Glu Arg Ile 2105	gac Asp 2110	ctt gag act gga ggg Leu Glu Thr Gly Gly 2110	aat cgc Asn Arg	7197
gag atg gtg Glu Met Val 2115	ctg tca gga agc Leu Ser Gly Ser 2120	aat Asn 2125	gtg gat atg ttt tca Val Asp Met Phe Ser 2125	gtc gca Val Ala	7242
gtc ttt ggg Val Phe Gly 2130	gct tac atc tac Ala Tyr Ile Tyr 2135	tgg Trp 2135	tct gac aga gca cat Ser Asp Arg Ala His 2140	gca aac Ala Asn	7287
ggg tct gtc Gly Ser Val 2145	aga agg ggc Arg Arg Gly His 2150	cac His 2150	aag aat gat gcc Lys Asn Asp Ala Thr 2155	acg ata Glu Thr Ile	7332
acc atg aga Thr Met Arg 2160	acc ggc ctt Thr Gly Leu Gly 2165	gga gtc Val 2165	aac ctg aag gag Asn Leu Lys Glu Val 2170	aaa ata Lys Ile	7377
ttt aac cga Phe Asn Arg 2175	gta aga gag aaa Val Arg Glu Lys 2180	ggg Gly 2180	acc aat gtt tgt Thr Asn Val Cys 2185	agg gac Arg Asp	7422
aat ggt ggc Asn Gly Gly 2190	tgt aag caa ctc Cys Lys Gln Leu 2195	tgt Cys 2195	ctt tat cga gga Leu Tyr Arg Gly 2200	tcc cgg Ser Arg	7467
aga act tgt Arg Thr 2205	gct tgt gcc cat Ala Cys Ala His 2210	gga Gly 2210	tat ttg gca gaa gat Tyr Leu Ala Glu Asp 2215	gga gtt Gly Val	7512
act tgc ctg Thr Cys Leu 2220	agg cat gaa ggc Arg His Glu Gly 2225	tat Tyr 2225	tta ctg tat tca gga Leu Leu Tyr Ser Gly 2230	aga aca Arg Thr	7557
ata tta aaa Ile Leu Lys 2235	agt ata cat ctt Ser Ile His Leu Ser 2240	tct Ser 2240	gat gaa acc aat Asp Glu Thr Asn Leu 2245	aat tcc Asn Ser	7602
cca ata agg Pro Ile Arg 2250	cca tat gag aat Pro Tyr Glu Asn Pro 2255	cca Pro 2255	cgt tat ttc aag aat Arg Tyr Phe Lys Asn 2260	gtc ata Val Ile	7647
gcc ttg gct Ala Leu Ala 2265	ttt gac tat aat Phe Asp Tyr Asn Gln 2270	caa Gln 2270	aga aga aaa ggt acc Arg Arg Lys Gly Thr 2275	aac cga Asn Arg	7692
atc ttt tac Ile Phe Tyr 2280	agt gat gca cac Ser Asp Ala His 2285	ttt Phe 2285	gga aat ata cag ctt Gly Asn Ile Gln Thr 2290	att aaa Ile Lys	7737
gac aac tgg Asp Asn Trp 2295	gaa gac aga caa Glu Asp Arg Gln 2300	gta Gln 2300	att gtt gaa aat Ile Val Glu Asn Val 2305	ggt tct Gly Ser	7782
gtg gaa gga Val Glu Gly 2310	ctt gcc tat cac Leu Ala Tyr His Arg 2315	aga Arg 2315	gcc tgg gat aca ctg Ala Trp Asp Thr Leu 2320	tac tgg Tyr Trp	7827
aca agc tct Thr Ser Ser 2325	acc acc tca tcc Thr Thr Ser Ser 2330	alc Ser 2330	acc aga cac act Thr Arg His Thr Val 2335	gac cag Asp Gln	7872

act cgg cct gga gca ttt gac agg gaa gct gtc atc acc atg tca	7917
Thr Arg Pro Gly Ala Phe Asp Arg Glu Ala Val Ile Thr Met Ser	
2340 2345 2350	
gaa gat gac cat cca cat gtg cta gcc ttg gat gaa tgt caa aat	7962
Glu Asp Asp His Pro His Val Leu Ala Leu Asp Glu Cys Gln Asn	
2355 2360 2365	
tta atg ttt tgg acc aac tgg aat gaa caa cat cca agt atc atg	8007
Leu Met Phe Trp Thr Asn Trp Asn Glu Gln His Pro Ser Ile Met	
2370 2375 2380	
aga tct act ctg act ggg aaa aat gct caa gtg gtg gtc agt aca	8052
Arg Ser Thr Leu Thr Gly Lys Asn Ala Gln Val Val Val Ser Thr	
2385 2390 2395	
gac ata ctc act cca aat gga ctt act atc gac tac cgt gca gag	8097
Asp Ile Leu Thr Pro Asn Gly Leu Thr Ile Asp Tyr Arg Ala Glu	
2400 2405 2410	
aag ctg tat ttc tca gat gcc agt cta gga aaa att gaa agg tgt	8142
Lys Leu Tyr Phe Ser Asp Gly Ser Leu Gly Lys Ile Glu Arg Cys	
2415 2420 2425	
gaa tac gat gga tcc cag aga cat gtg ata gtt aaa tct ggg cca	8187
Glu Tyr Asp Gly Ser Gln Arg His Val Ile Val Lys Ser Gly Pro	
2430 2435 2440	
ggg act ttc ctc agt ttg gct gtt tat gac aat tat ata ttc tgg	8232
Gly Thr Phe Leu Ser Leu Ala Val Tyr Asp Asn Tyr Ile Phe Trp	
2445 2450 2455	
tcg gac tgg gga aga aga gct ata ctg cgg tcc aac aag tac aca	8277
Ser Asp Trp Gly Arg Arg Ala Ile Leu Arg Ser Asn Lys Tyr Thr	
2460 2465 2470	
gga gga gat aca aaa att ctt cgt tcc gat att cca cat cag cca	8322
Gly Gly Asp Thr Lys Ile Leu Arg Ser Asp Ile Pro His Gln Pro	
2475 2480 2485	
atg gga atc ata gct gtt gcc aat gac acc aat agc tgt gaa ctt	8367
Met Gly Ile Ile Ala Val Ala Asn Asp Thr Asn Ser Cys Glu Leu	
2490 2495 2500	
tct cca tgt gca tta ttg aat gga gcc tgc cat gac ttg tgc ctt	8412
Ser Pro Cys Ala Leu Leu Asn Gly Gly Cys His Asp Leu Cys Leu	
2505 2510 2515	
tta act ccc aat ggg aga gtg aat tgt tcc tgc aga ggg gac cga	8457
Leu Thr Pro Asn Gly Arg Val Asn Cys Ser Cys Arg Gly Asp Arg	
2520 2525 2530	
ata ttg cta gag gac aac aga tgt gtg act aaa aat tcc tcc tgc	8502
Ile Leu Leu Glu Asp Asn Arg Cys Val Thr Lys Asn Ser Ser Cys	
2535 2540 2545	
aac gct tat tcg gag ttt gaa tgt gga aat ggt gag tgc att gac	8547
Asn Ala Tyr Ser Glu Phe Glu Cys Gly Asn Gly Glu Cys Ile Asp	
2550 2555 2560	
tac cag ctc acc tgt gat gcc att cct cac tgt aaa gat aaa tca	8592
Tyr Gln Leu Thr Cys Asp Gly Ile Pro His Cys Lys Asp Lys Ser	
2565 2570 2575	

gat gaa aaa	ctg ctc tac	tgt gaa	aac aga agc	tgt cga	aga ggc	8637
Asp Glu Lys	Leu Leu Tyr Cys	Glu	Asn Arg Ser Cys	Arg	Gly	
2580		2585		2590		
ttc aag cca	tgc tat aat	cgc cgc	tgc att cct	cat ggc	aag tta	8682
Phe Lys Pro	Cys Tyr Asn Arg	Arg	Cys Ile Pro His	Gly	Lys Leu	
2595		2600		2605		
tgt gat gga	gaa aat gac	tgc gga	gac aac tct	gat gaa	tta gat	8727
Cys Asp Gly	Glu Asn Asp Cys	Gly	Asp Asn Ser Asp	Glu	Leu Asp	
2610		2615		2620		
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Cys Lys Val	Ser Thr Cys Ala	Thr	Val Glu Phe Arg	Cys	Ala Asp	
2625		2630		2635		
ggg act tgt	att cca aga	tca gca	cga tgc aac	cag aac	ata gat	8817
Gly Thr Cys	Ile Pro Arg Ser	Ala	Arg Cys Asn Gln	Asn	Ile Asp	
2640		2645		2650		
tgt gca gat	gct tca gat	gaa aag	aac tgc aat	aac aca	gac tgc	8862
Cys Ala Asp	Ala Ser Asp Glu	Lys	Asn Cys Asn Asn	Thr	Asp Cys	
2655		2660		2665		
aca cat ttc	tat aag ctt	gga gtg	aaa acc aca	ggg ttc	ata aga	8907
Thr His Phe	Tyr Lys Leu Gly	Val	Lys Thr Thr Gly	Phe	ile Arg	
2670		2675		2680		
tgt aat tct	acc tca ctg	tgt gtt	ctg cca acc	tgg ata	tgc gac	8952
Cys Asn Ser	Thr Ser Leu Cys	Val	Leu Pro Thr Trp	ile	Cys Asp	
2685		2690		2695		
ggg tct aat	gac tgt gga	gac tat	tca gat gaa	tta aag	tgc cca	8997
Gly Ser Asn	Asp Cys Gly Asp	Tyr	Ser Asp Glu Leu	Lys	Cys Pro	
2700		2705		2710		
gtt cag aac	aaa cac aaa	tgt gaa	gaa aat tat	ttt agt	tgt cct	9042
Val Gln Asn	Lys His Lys Cys	Glu	Glu Asn Tyr Phe	Ser	Cys Pro	
2715		2720		2725		
agt gga aga	tgc att ttg	aat acc	tgg ata tgc	gat ggt	cag aaa	9087
Ser Gly Arg	Cys Ile Leu Asn	Thr	Trp Ile Cys Asp	Gly	Gln Lys	
2730		2735		2740		
gat tgt gag	gat gga cgt	gat gaa	ttc cac tgt	gat tct	tct tgc	9132
Asp Cys Glu	Asp Gly Arg Asp	Glu	Phe His Cys Asp	Ser	Ser Cys	
2745		2750		2755		
tct tgg aac	caa ttt gct	tgt tcc	gca caa aaa	tgt att	tct aag	9177
Ser Trp Asn	Gln Phe Ala Cys	Ser	Ala Gln Lys Cys	ile	Ser Lys	
2760		2765		2770		
cat tgg att	tgt gat gga	gaa gat	gac tgt ggg	gat ggg	tta gat	9222
His Trp Ile	Cys Asp Gly Glu	Asp	Asp Cys Gly Asp	Gly	Leu Asp	
2775		2780		2785		
gaa agt gac	agc att tgt	ggt gcc	ata acc tgt	gct gct	gac atg	9267
Glu Ser Asp	Ser Ile Cys Gly	Ala	ile Thr Cys Ala	Ala	Asp Met	
2790		2795		2800		
ttc agc tgc	cag ggc tct	cgt gcc	tgc gtg ccc	cga cat	tgg ctt	9312
Phe Ser Cys	Gln Gly Ser Arg	Ala	Cys Val Pro Arg	His	Trp Leu	
2805		2810		2815		

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2820 2825 2830	
aca gca ggc tgc gct ccc aat aat aca tgt gat gaa aat gct ttc Thr Ala Gly Cys Ala Pro Asn Asn Thr Cys Asp Glu Asn Ala Phe	9402
2835 2840 2845	
atg tgc cat aat aaa gta tgc att ccc aag caa ttt gtt tgt gac Met Cys His Asn Lys Val Cys Ile Pro Lys Gln Phe Val Cys Asp	9447
2850 2855 2860	
cat gat gac gac tgt gga gat ggc tct gat gag tca ccg cag tgt His Asp Asp Asp Cys Gly Asp Gly Ser Asp Glu Ser Pro Gln Cys	9492
2865 2870 2875	
gga tac cga cag tgt ggt aca gaa ttt agt tgt gct gat ggg Gly Tyr Arg Gln Cys Gly Thr Glu Glu Phe Ser Cys Ala Asp Gly	9537
2880 2885 2890	
cgg tgt ctt cta aat act caa tgg cag tgt gat gga gac ttt gac Arg Cys Leu Leu Asn Thr Gln Trp Gln Cys Asp Gly Asp Phe Asp	9582
2895 2900 2905	
tgt cct gac cat tct gat gaa gca cct tta aac cca aag tgt aaa Cys Pro Asp His Ser Asp Glu Ala Lys Pro Leu Asn Pro Cys Lys	9627
2910 2915 2920	
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2925 2930 2935	
ggc agg tgc att ccc agt gga ggt ctt tgt gac aat aag gat gac Gly Arg Cys Ile Pro Ser Gly Gly Leu Cys Asp Asn Lys Asp Asp	9717
2940 2945 2950	
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2955 2960 2965	
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2970 2975 2980	
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2985 2990 2995	
gat gac ggc aaa aca tgt gta gac att gat gaa tgc tct cca ggc Asp Asp Gly Lys Thr Cys Val Asp Ile Asp Glu Cys Ser Ser Gly	9897
3000 3005 3010	
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3015 3020 3025	
tgc ctc tgt aca gat ggg tat gaa ata caa cct gat aac cca aat Cys Leu Cys Thr Asp Gly Tyr Glu Ile Gln Pro Asp Asn Pro Asn	9987
3030 3035 3040	
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3045 3050 3055	

gat cat cat gag ata agg aaa att agc act gat ggc tcc aac tac	10077
Asp His His Glu Ile Arg Lys Ile Ser Thr Asp Gly Ser Asn Tyr	
3060 3065 3070	
aca ctt tta aaa cag gga tta aac aat gtt att gct ata gac ttt	10122
Thr Leu Leu Lys Gln Gly Leu Asn Asn Val Ile Ala Ile Asp Phe	
3075 3080 3085	
gat tac aga gaa gaa ttc atc tat tgg atc gat tct agc cga ccc	10167
Asp Tyr Arg Glu Glu Phe Ile Tyr Trp Ile Asp Ser Ser Arg Pro	
3090 3095 3100	
aat ggc agt cgc ata aat aga atg tgt tta aat gga agt gac att	10212
Asn Gly Ser Arg Ile Asn Arg Met Cys Leu Asn Gly Ser Asp Ile	
3105 3110 3115	
aag gta gtt cat aac aca gcg gtc ccc aat gca ctt gct gtc gat	10257
Lys Val Val His Asn Thr Ala Val Pro Asn Ala Leu Ala Val Asp	
3120 3125 3130	
tgg att gga aaa aac ctc tat tgg tct gac aca gaa aaa aga atc	10302
Trp Ile Gly Lys Asn Leu Tyr Trp Ser Asp Thr Glu Lys Arg Ile	
3135 3140 3145	
att gaa gta tcc aaa ctc aat ggc ttg tac cct act ata ctc gtt	10347
Ile Glu Val Ser Lys Leu Asn Gly Leu Tyr Pro Thr Ile Leu Val	
3150 3155 3160	
agc aaa agg ctg aag ttt ccc aga gac ttg tct tta gat cct caa	10392
Ser Lys Arg Leu Lys Phe Pro Arg Asp Leu Ser Leu Asp Pro Gln	
3165 3170 3175	
gct gga tat ttg tat tgg att gac tgc tgc gag tat cct cat att	10437
Ala Gly Tyr Leu Tyr Trp Ile Asp Cys Cys Glu Tyr Pro His Ile	
3180 3185 3190	
ggc cgt gtt gga atg gat gga acc aat cag agt gtt gtc ata gaa	10482
Gly Arg Val Gly Met Asp Gly Thr Asn Gln Ser Val Val Ile Glu	
3195 3200 3205	
acc aag att tct aga cct atg gca cta aca ata gat tat gtt aat	10527
Thr Lys Ile Ser Arg Pro Met Ala Leu Thr Ile Asp Tyr Val Asn	
3210 3215 3220	
cgt aga ctc tac tgg gcc gat gaa aat cac att gaa ttt agc aac	10572
Arg Arg Leu Tyr Trp Ala Asp Glu Asn His Ile Glu Phe Ser Asn	
3225 3230 3235	
atg gat gga tct cat aga cac aaa gtc cct aat caa gat att cca	10617
Met Asp Gly Ser His Arg His Lys Val Pro Asn Gln Asp Ile Pro	
3240 3245 3250	
ggg gtg att gca cta aca ttg ttt gaa gac tac atc tac tgg act	10662
Gly Val Ile Ala Leu Thr Leu Phe Glu Asp Tyr Ile Tyr Trp Thr	
3255 3260 3265	
gat ggg aaa acc aag tca ctc agc cgt gcc cat aaa aca tgc gga	10707
Asp Gly Lys Thr Lys Ser Leu Ser Arg Ala His Lys Thr Ser Gly	
3270 3275 3280	
gca gac aga ctc tca ctg att tac tca tgg cat gcc atc aca gat	10752
Ala Asp Arg Leu Ser Leu Ile Tyr Ser Trp His Ala Ile Thr Asp	
3285 3290 3295	

atc	cag	gtg	tat	cat	tct	tat	aga	caa	cct	gat	gtc	tcc	aaa	cat	10797
Ile	Gln	Val	Tyr	His	Ser	Tyr	Arg	Gln	Pro	Asp	Val	Ser	Lys	His	
		3300					3305					3310			
ctc	tgc	atg	ata	aat	aat	ggg	ggg	tgc	agt	cat	ttg	tgc	ctt	tta	10842
Leu	Cys	Met	Ile	Asn	Asn	Gly	Gly	Cys	Ser	His	Leu	Cys	Leu	Leu	
		3315					3320					3325			
gcc	cct	gga	aaa	acc	cac	act	tgt	gca	tgt	ccc	act	aac	ttc	tat	10887
Ala	Pro	Gly	Lys	Thr	His	Thr	Cys	Ala	Cys	Pro	Thr	Asn	Phe	Tyr	
		3330					3335					3340			
ctg	gca	gct	gat	aat	agg	act	tgc	tta	tcc	aac	tgc	aca	gcc	ggc	10932
Leu	Ala	Ala	Asp	Asn	Arg	Thr	Cys	Leu	Ser	Asn	Cys	Thr	Ala	Ser	
		3345					3350					3355			
cag	ttt	cgt	tgc	aaa	act	gac	aaa	tgt	att	cca	ttc	tgg	tgg	aaa	10977
Gln	Phe	Arg	Cys	Lys	Thr	Asp	Lys	Cys	Ile	Pro	Phe	Trp	Trp	Lys	
		3360					3365					3370			
tgt	gac	acc	gtg	gat	gac	tgt	ggg	gat	gga	tct	gat	gaa	cct	gat	11022
Cys	Asp	Thr	Val	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Pro	Asp	
		3375					3380					3385			
gac	tgt	cct	gaa	ttt	aga	tgt	cag	cca	ggc	cga	ttt	cag	tgt	ggg	11067
Asp	Cys	Pro	Glu	Phe	Arg	Cys	Gln	Pro	Gly	Arg	Phe	Gln	Cys	Gly	
		3390					3395					3400			
act	gga	ctc	tgt	gct	cta	cca	gct	ttc	atc	tgt	gat	gga	gag	aat	11112
Thr	Gly	Leu	Cys	Ala	Leu	Pro	Ala	Phe	Ile	Cys	Asp	Gly	Glu	Asn	
		3405					3410					3415			
gat	tgt	gga	gac	aat	tct	gat	gaa	ctc	aac	tgt	gac	aca	cat	gtc	11157
Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Leu	Asn	Cys	Asp	Thr	His	Val	
		3420					3425					3430			
tgc	ctg	tca	ggg	caa	ttc	aaa	tgt	acc	aag	aac	cag	aaa	tgt	atc	11202
Cys	Leu	Ser	Gly	Gln	Phe	Lys	Cys	Thr	Lys	Asn	Gln	Lys	Cys	Ile	
		3435					3440					3445			
cca	gta	aac	tta	aga	tgt	aat	ggg	caa	gat	gac	tgt	ggg	gat	gag	11247
Pro	Val	Asn	Leu	Arg	Cys	Asn	Gly	Gln	Asp	Asp	Cys	Gly	Asp	Glu	
		3450					3455					3460			
gaa	gat	gaa	aga	gac	tgt	cct	gaa	aac	agc	tgt	tct	cca	gac	tat	11292
Glu	Asp	Glu	Arg	Asp	Cys	Pro	Glu	Asn	Ser	Cys	Ser	Pro	Asp	Tyr	
		3465					3470					3475			
ttc	cag	tgt	aag	act	acg	aag	cat	tgc	att	tcc	aag	ctg	tgg	gtt	11337
Phe	Gln	Cys	Lys	Thr	Thr	Lys	His	Cys	Ile	Ser	Lys	Leu	Trp	Val	
		3480					3485					3490			
tgt	gac	gag	gat	cca	gac	tgt	gca	gat	gca	tca	gac	gag	gcc	aac	11382
Cys	Asp	Glu	Asp	Pro	Asp	Cys	Ala	Asp	Ala	Ser	Asp	Glu	Ala	Asn	
		3495					3500					3505			
tgc	gat	aaa	aag	act	tgt	gga	cct	cat	gaa	ttc	cag	tgt	aaa	aac	11427
Cys	Asp	Lys	Lys	Thr	Cys	Gly	Pro	His	Glu	Phe	Gln	Cys	Lys	Asn	
		3510					3515					3520			
aac	aac	tgt	att	ccc	gat	cac	tgg	cgg	tgt	gat	agc	caa	aat	gac	11472
Asn	Asn	Cys	Ile	Pro	Asp	His	Trp	Arg	Cys	Asp	Ser	Gln	Asn	Asp	
		3525					3530					3535			

tgc agt gat Cys Ser Asp 3540	aat tca gat gaa Asn Ser Asp Glu 3545	gaa aac tgt aag cca Glu Asn Cys Lys Pro 3550	cag aca tgt Gln Thr Cys 3555	11517
aca ttg aaa Thr Leu Lys 3555	gat ttc ctc tgt Asp Phe Leu Cys 3560	gcc aat ggg gac tgt Ala Asn Gly Asp Cys 3565	gtt tct tca Val Ser Ser 3570	11562
agg ttt tgg Arg Phe Trp 3570	tgt gat gga gat Cys Asp Gly Asp 3575	ttt gac tgt gca Phe Asp Cys Ala 3580	gat ggc tct Gly Ser Asp 3585	11607
gag aga aat Glu Arg Asn 3585	tgt gag aca agt Cys Glu Thr Ser 3590	tcc aaa gat Ser Lys Asp 3595	cag ttc cgg Gln Phe Arg 3600	11652
tcc aat ggt Ser Asn Gly 3600	cag tgt ata Gln Cys Ile Pro 3605	gca aaa tgg Ala Lys Trp 3610	aaa tgt gat Lys Cys Asp 3615	11697
gaa gac tgc Glu Asp Cys 3615	aaa tat ggg Lys Tyr Gly 3620	gaa gat gag Glu Asp Lys 3625	agc tgt gga Ser Cys Pro 3630	11742
tct cct act Ser Pro Thr 3630	tgc tca tca Cys Ser Ser 3635	cgt gaa Arg Glu Tyr 3640	tat ata tgt Ile Cys Ala 3645	11787
tgt att tca Cys Ile Ser 3645	gca tct ttg Ala Ser Leu 3650	aaa tgt Lys Cys 3655	aat gga gaa Asn Gly Glu 3660	11832
gat ggt tca Asp Gly Ser 3660	gat gag atg Asp Glu Met 3665	gac tgt Asp Cys 3670	gtg act gaa Val Thr Glu 3675	11877
cag ttt cgg Gln Phe Arg 3675	tgc aaa aat Cys Lys Asn 3680	aaa gcc Lys Ala 3685	cac tgt att His Cys Ile 3690	11922
ctg tgt gat Leu Cys Asp 3690	gga att cat Gly Ile His 3695	gac tgt Asp Cys 3700	gtg gat ggc Val Asp Gly 3705	11967
aac tgt gaa Asn Cys Glu 3705	aga gga gga Arg Gly Gly 3710	aat ata Asn Ile 3715	tgt aga gct Cys Arg Ala 3720	12012
tgc aat aat Cys Asn Ser 3720	tct ctc tgc Ser Leu Cys 3725	aaa cta Lys Leu 3730	cat ttc tgg His Phe Trp 3735	12057
gag gac gac Glu Asp Asp 3735	tgt gga gac Cys Gly Asp 3740	aac tct Asn Ser 3745	gat gaa gcc Asp Glu Ala 3750	12102
gtc aaa ttt Val Lys Phe 3750	ctt tgt cca Leu Cys Pro 3755	tcc acg Ser Thr 3760	aga cct cac Arg Pro His 3765	12147
aac aga ata Asn Arg Ile 3765	tgc cta cag Cys Leu Gln 3770	tcg gag Ser Glu 3775	caa atg tgc Gln Met Cys 3780	12192

gaa tgc ggt gac aat tca gat gaa gat cac tgt ggt ggt aag ctg	12237
Glu Cys Gly Asp Asn Ser Asp Glu Asp His Cys Gly Gly Lys Leu	
3780 3785 3790	
aca tat aaa gca agg cct tgt aaa aag gat gag ttt gct tgt agt	12282
Thr Tyr Lys Ala Arg Pro Cys Lys Lys Asp Glu Phe Ala Cys Ser	
3795 3800 3805	
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Asn Lys Lys Cys Ile Pro Met Asp Leu Gln Cys Asp Arg Leu Asp	
3810 3815 3820	
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Asp Cys Gly Asp Gly Ser Asp Glu Gln Gly Cys Arg Ile Ala Pro	
3825 3830	
act gaa tat acc tgt gaa gat aat gtg aat cca tgt gga gat gat	12417
Thr Glu Tyr Thr Cys Glu Asp Asn Val Asn Pro Cys Gly Asp Asp	
3840 3845 3850	
gca tat tgt aat caa ata aaa aca tct gtt ttc tgt cgc tgt aag	12462
Ala Tyr Cys Asn Gln Ile Lys Thr Ser Val Phe Cys Arg Cys Lys	
3855 3860 3865	
cct gga ttt cag aga aac atg aaa aac aga caa tgt gaa gac ctt	12507
Pro Gly Phe Gln Arg Asn Met Lys Asn Arg Gln Cys Glu Asp Leu	
3870 3875 3880	
aat gaa tgt ttg gtg ttt ggc aca tgt tcc cat caa tgt ata aat	12552
Asn Glu Cys Leu Val Phe Gly Thr Cys Ser His Gln Tgt Ile Asn	
3885 3890 3895	
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Val Glu Gly Ser Tyr Lys Cys Val Phe Cys Asp Gln Asn Gln Glu	
3900 3905 3910	
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Arg Asn Asn Thr Cys Ile Ala Glu Gly Ser Glu Asp Gln Val Leu	
3915 3920 3925	
tac att gct aat gac act gat atc ctg ggt ttt ata tat cca ttc	12687
Tyr Ile Ala Asn Asp Thr Asp Ile Leu Gly Phe Ile Tyr Pro Phe	
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aac tac agt ggc gat cat caa caa att tct cat att gaa cat aat	12732
Asn Tyr Ser Gly Asp His Gln Gln Ile Ser His Ile Glu His Asn	
3945 3950 3955	
tca aga ata aca ggg atg gat gta tat tat caa aga gat atg att	12777
Ser Arg Ile Thr Gly Met Asp Val Tyr Tyr Gln Arg Asp Met Ile	
3960 3965 3970	
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Ile Trp Ser Thr Gln Phe Asn Pro Gly Gly Ile Phe Tyr Lys Arg	
3975 3980 3985	
atc cat ggc aga gaa aaa agg caa gca aac agt ggc ttg att tgt	12867
Ile His Gly Arg Glu Lys Arg Gln Ala Asn Ser Gly Leu Ile Cys	
3990 3995 4000	
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Pro Glu Phe Lys Arg Pro Arg Asp Ile Ala Val Asp Trp Val Ala	
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Gly Asn Ile	Tyr Trp Thr	Asp His	Ser Arg Met	His Trp	Phe Ser	
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Tyr Tyr Thr	Thr His Trp Thr	Ser Leu	Arg Tyr Ser	Ile Asn Val		
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Gly Gln Leu	Asn Gly Pro Asn	Cys Thr	Arg Leu Thr	Thr Asn Met		
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Ala Gly Glu	Pro Tyr Ala Ile	Ala Val	Asn Pro Lys	Arg Gly Met		
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Met Tyr Trp	Thr Val Val Gly	Asp His	Ser His Ile	Glu Glu Ala		
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Ala Met Asp	Gly Thr Leu Arg	Arg Ile	Leu Val Gln	Lys Asn Leu		
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Gln Arg Pro	Thr Gly Leu Ala	Val Asp	Tyr Phe Ser	Glu Arg Ile		
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Tyr Trp Ala	Asp Phe Glu Leu	Ser Ile	Ile Gly Ser	Val Leu Tyr		
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Asp Gly Ser	Asn Ser Val Val	Ser Val	Ser Ser Lys	Gln Gly Leu		
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tta cat cca	cat agg atc gat	atc ttt	gaa gat tat	ata tat gga	13362	
Leu His Pro	His Arg Ile Asp	Ile Phe	Glu Asp Tyr	Ile Tyr Gly		
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Ala Gly Pro	Lys Asn Gly Val	Phe Arg	Val Gln Lys	Gly Gly His		
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Gly Ser Val	Glu Tyr Leu Ala	Leu Asn	Ile Asp Lys	Thr Lys Gly		
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Val Leu Ile	Ser His Arg Tyr	Lys Gln	Leu Asp Leu	Pro Asn Pro		
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Cys Leu Asp	Leu Ala Cys Glu	Phe Leu	Cys Leu Leu	Asn Pro Ser		
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Gly Ala Thr	Cys Val Cys Pro	Glu Gly	Lys Tyr Leu	Ile Asn Gly		
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acc tgc aat	gat gac agc ctg	tta gat	gat tca tgt	aag tta act	13632	
Thr Cys Asn	Asp Asp Ser Leu	Leu Asp	Asp Ser Cys	Lys Leu Thr		
4245		4250		4255		

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Cys Glu Asn Gly Gly Arg Cys Ile Leu Asn Glu Lys Gly Asp Leu	
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Arg Cys His Cys Trp Pro Ser Tyr Ser Gly Glu Arg Cys Glu Val	
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Asn His Cys Ser Asn Tyr Cys Gln Asn Gly Gly Thr Cys Val Pro	
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Ser Val Leu Gly Arg Pro Thr Cys Ser Cys Ala Leu Gly Phe Thr	
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Cys Gln Pro Glu Tyr Thr Gly Asp Arg Cys Gln Tyr Tyr Val Cys	
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Cys Glu Val Asp Lys Cys Val Arg Cys His Gly Gly His Cys Ile	
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Pro Lys Ser Ser Lys Ser Asp His Ile Ser Thr Arg Ser Ile Ala	
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Ile Ile Val Pro Leu Val Leu Leu Val Thr Leu Ile Thr Thr Leu	
4485 4490 4495	

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Val Ile Gly Leu Val Leu Cys Lys	Arg Lys Arg Arg Thr	Lys Thr	
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Gly Asn Pro Ser Tyr Asn Met Tyr	Glu Val Asp His Asp	His Asn	
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Asp Gly Gly Leu Leu Asp Pro Gly	Phe Met Ile Asp Pro	Thr Lys	
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gcc agg tac ata ggg gga gga ccc	agt gct ttc aag ctt	cca cac	14577
Ala Arg Tyr Ile Gly Gly Gly Pro	Ser Ala Phe Lys Leu	Pro His	
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Thr Ala Pro Pro Ile Tyr Leu Asn	Ser Asp Leu Lys Gly	Pro Leu	
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Thr Ala Gly Pro Thr Asn Tyr Ser	Asn Pro Val Tyr Ala	Lys Leu	
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Tyr Met Asp Gly Gln Asn Cys Arg	Asn Ser Leu Gly Ser	Val Asp	
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<212> PRT
<213> Homo sapiens

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<400> 33

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Ala Ala Gly Pro Lys Val Pro Pro Ser Ser Leu Gln Arg Arg Leu Pro
20          25          30

```

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Tyr Arg Ala Thr Thr Met Ser Glu Phe Leu Leu Ala Leu Leu Thr Leu
35          40          45

```

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Ser Gly Leu Leu Pro Ile Ala Arg Val Leu Thr Val Gly Ala Asp Arg
50          55          60

```

```

Asp Gln Gln Leu Cys Asp Pro Gly Glu Phe Leu Cys His Asp His Val
65          70          75          80

```

```

Thr Cys Val Ser Arg Ser Trp Leu Cys Asp Gly Asp Pro Asp Cys Pro

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85										90					95				
Asp	Asp	Ser	Asp	Glu	Ser	Leu	Asp	Thr	Cys	Pro	Glu	Glu	Val	Glu	Ile				
			100					105						110					
Lys	Cys	Pro	Leu	Asn	His	Ile	Ala	Cys	Leu	Gly	Thr	Asn	Lys	Cys	Val				
		115					120					125							
His	Leu	Ser	Gln	Leu	Cys	Asn	Gly	Val	Leu	Asp	Cys	Pro	Asp	Gly	Tyr				
	130					135					140								
Asp	Glu	Gly	Val	His	Cys	Gln	Glu	Leu	Leu	Ser	Asn	Cys	Gln	Gln	Leu				
145					150					155					160				
Asn	Cys	Gln	Tyr	Lys	Cys	Thr	Met	Val	Arg	Asn	Ser	Thr	Arg	Cys	Tyr				
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Cys	Glu	Asp	Gly	Phe	Glu	Ile	Thr	Glu	Asp	Gly	Arg	Ser	Cys	Lys	Asp				
			180					185					190						
Gln	Asp	Glu	Cys	Ala	Val	Tyr	Gly	Thr	Cys	Ser	Gln	Thr	Cys	Arg	Asn				
		195					200						205						
Thr	His	Gly	Ser	Tyr	Thr	Cys	Ser	Cys	Val	Glu	Gly	Tyr	Leu	Met	Gln				
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Pro	Asp	Asn	Arg	Ser	Cys	Lys	Ala	Lys	Ile	Glu	Pro	Thr	Asp	Arg	Pro				
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Pro	Ile	Leu	Leu	Ile	Ala	Asn	Phe	Glu	Thr	Ile	Glu	Val	Phe	Tyr	Leu				
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Asn	Gly	Ser	Lys	Met	Ala	Thr	Leu	Ser	Ser	Val	Asn	Gly	Asn	Glu	Ile				
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His	Thr	Leu	Asp	Phe	Ile	Tyr	Asn	Glu	Asp	Val	Ile	Cys	Trp	Ile	Glu				
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Ser	Arg	Glu	Ser	Ser	Asn	Gln	Leu	Lys	Cys	Ile	Gln	Ile	Thr	Lys	Ala				
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Gly	Gly	Leu	Thr	Asp	Glu	Trp	Thr	Ile	Asn	Ile	Leu	Gln	Ser	Phe	His				
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Val Asp His Val Gly Asp Arg Ile Phe Val Cys Asn Ser Asn Gly Ser
340 345 350

Val Cys Val Thr Leu Ile Asp Leu Glu Leu His Asn Pro Lys Ala Ile
355 360 365

Ala Val Asp Pro Ile Ala Gly Lys Leu Phe Phe Thr Asp Tyr Gly Asn
370 375 380

Val Ala Lys Val Glu Arg Cys Asp Met Asp Gly Met Asn Arg Thr Arg
385 390 395 400

Ile Ile Asp Ser Lys Thr Glu Gln Pro Ala Ala Leu Ala Leu Asp Leu
405 410 415

Val Asn Lys Leu Val Tyr Trp Val Asp Leu Tyr Leu Asp Tyr Val Gly
420 425 430

Val Val Asp Tyr Gln Gly Lys Asn Arg His Thr Val Ile Gln Gly Arg
435 440 445

Gln Val Arg His Leu Tyr Gly Ile Thr Val Phe Glu Asp Tyr Leu Tyr
450 455 460

Ala Thr Asn Ser Asp Asn Tyr Asn Ile Val Arg Ile Asn Arg Phe Asn
465 470 475 480

Gly Thr Asp Ile His Ser Leu Ile Lys Ile Glu Asn Ala Trp Gly Ile
485 490 495

Arg Ile Tyr Gln Lys Arg Thr Gln Pro Thr Val Arg Ser His Ala Cys
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Glu Val Asp Pro Tyr Gly Met Pro Gly Gly Cys Ser His Ile Cys Leu
515 520 525

Leu Ser Ser Ser Tyr Lys Thr Arg Thr Cys Arg Cys Arg Thr Gly Phe
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Asn Leu Gly Ser Asp Gly Arg Ser Cys Lys Arg Pro Lys Asn Glu Leu
545 550 555 560

Phe Leu Phe Tyr Gly Lys Gly Arg Pro Gly Ile Val Arg Gly Met Asp
565 570 575

Leu Asn Thr Lys Ile Ala Asp Glu Tyr Met Ile Pro Ile Glu Asn Leu
580 585 590

Val Asn Pro Arg Ala Leu Asp Phe His Ala Glu Thr Asn Tyr Ile Tyr
595 600 605

Phe Ala Asp Thr Thr Ser Phe Leu Ile Gly Arg Gln Lys Ile Asp Gly
610 615 620

Thr Glu Arg Glu Thr Ile Leu Lys Asp Asp Leu Asp Asn Val Glu Gly
625 630 635 640

Ile Ala Val Asp Trp Ile Gly Asn Asn Leu Tyr Trp Thr Asn Asp Gly
645 650 655

His Arg Lys Thr Ile Asn Val Ala Arg Leu Glu Lys Ala Ser Gln Ser
660 665 670

Arg Lys Thr Leu Leu Glu Gly Glu Met Ser His Pro Arg Gly Ile Val
675 680 685

Val Asp Pro Ile Asn Gly Trp Met Tyr Trp Thr Asp Trp Glu Glu Asp
690 695 700

Glu Ile Asp Asp Ser Val Gly Arg Ile Glu Lys Ala Trp Met Asp Gly
705 710 715 720

Phe Asn Arg Gln Ile Phe Val Thr Ser Lys Met Leu Trp Pro Asn Gly
725 730 735

Leu Thr Leu Asp Phe His Thr Asn Thr Leu Tyr Trp Cys Asp Ala Tyr
740 745 750

Tyr Asp His Ile Glu Lys Val Phe Leu Asn Gly Thr His Arg Lys Ile
755 760 765

Val Tyr Ser Gly Arg Glu Leu Asn His Pro Phe Gly Leu Ser His His
770 775 780

Gly Asn Tyr Val Phe Trp Thr Asp Tyr Met Asn Gly Ser Ile Phe Gln
785 790 795 800

Leu Asp Leu Ile Thr Ser Glu Val Thr Leu Leu Arg His Glu Arg Pro
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Pro Leu Phe Gly Leu Gln Ile Tyr Asp Pro Arg Lys Gln Gln Gly Asp
820 825 830

Asn Met Cys Arg Val Asn Asn Gly Gly Cys Ser Thr Leu Cys Leu Ala
835 840 845

Ile Pro Gly Gly Arg Val Cys Ala Cys Ala Asp Asn Gln Leu Leu Asp
850 855 860

Glu Asn Gly Thr Thr Cys Thr Phe Asn Pro Gly Glu Ala Leu Pro His
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Ile Cys Lys Ala Gly Glu Phe Arg Cys Lys Asn Arg His Cys Ile Gln
885 890 895

Ala Arg Trp Lys Cys Asp Gly Asp Asp Cys Leu Asp Gly Ser Asp
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Glu Asp Ser Val Asn Cys Phe Asn His Ser Cys Pro Asp Asp Gln Phe
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Lys Cys Gln Asn Asn Arg Cys Ile Pro Lys Arg Trp Leu Cys Asp Gly
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Thr Asp Glu Met Ala Ser Cys Glu Phe Pro Thr Cys Glu Pro Leu Thr
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Gln Phe Val Cys Lys Ser Gly Arg Cys Ile Ser Ser Lys Trp His
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Cys Val His Ser Cys Phe Asp Asn Gln Phe Arg Cys Ser Ser Gly
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Ile His Ser Pro Ala Gly Cys Asn Gly Asn Glu Phe Gln Cys His
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Lys Asp	Cys Glu Asp Gly Ser	Asp Glu Lys Gly Cys	Asn Gly Thr
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Ile Arg	Leu Cys Asp His Lys	Thr Lys Phe Ser Cys	Trp Ser Thr
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Gly Arg	Cys Ile Asn Lys Ala	Trp Val Cys Asp Gly	Asp Ile Asp
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Cys Glu	Asp Gln Ser Asp Glu	Asp Asp Cys Asp Ser	Phe Leu Cys
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Gln Pro	Glu Lys Leu Cys Asn	Gly Lys Lys Asp Cys	Pro Asp Gly
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Ser Asp	Glu Gly Tyr Leu Cys	Asp Glu Cys Ser Leu	Asn Asn Gly
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Gly Cys	Ser Asn His Cys Ser	Val Val Pro Gly Arg	Gly Ile Val
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Cys Ser	Cys Pro Glu Gly Leu	Gln Leu Asn Lys Asp	Asn Lys Thr
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Cys Glu	Ile Val Asp Tyr Cys	Ser Asn His Leu Lys	Cys Ser Gln
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Val Cys	Glu Gln His Lys His	Thr Val Lys Cys Ser	Cys Tyr Glu
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Gly Trp	Lys Leu Asp Val Asp	Gly Glu Ser Cys Thr	Ser Val Asp
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Pro Phe	Glu Ala Phe Ile Ile	Phe Ser Ile Arg His	Glu Ile Arg
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Arg Ile	Asp Leu His Lys Arg	Asp Tyr Ser Leu Leu	Val Pro Gly
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Ala Lys	Leu Asp Gly Ser	Leu	Arg Thr Thr Leu	Ile Ala Gly Ala
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Met Glu	His Pro Arg Ala	Ile	Ala Leu Asp Pro Arg	Tyr Gly Ile
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Ala Ser	Met Ser Gly Ala	Gly	Arg Lys Thr Ile Tyr	Lys Asp Met
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Lys Arg	Ile Val Trp Thr	Asp	Ala Arg Ser Asp	Ile Tyr Ser
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Ala Leu	Tyr Asp Gly Thr	Asn	Met Ile Glu Ile	Ile Arg Gly His
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Glu Tyr	Leu Ser His Pro	Phe	Ala Val Ser Leu Tyr	Gly Ser Glu
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Val Tyr	Trp Thr Asp Trp	Arg	Thr Asn Thr Leu Ser	Lys Ala Asn
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Lys Trp	Thr Gly Gln Asn	Val	Ser Val Ile Gln Lys	Thr Ser Ala
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Gln Pro	Phe Asp Leu Gln	Ile	Tyr His Pro Ser Arg	Gln Pro Gln
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Ala Pro	Asn Pro Cys Ala	Ala	Asn Asp Gly Lys Gly	Pro Cys Ser
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Leu Tyr	Trp Thr Asp Gly	Asn	Thr Ile Asn Met	Ala	Asn Met Asp
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Gly Ser	Asn Ser Lys Ile	Leu	Phe Gln Asn Gln	Lys	Glu Pro Val
1760		1765		1770	
Gly Leu	Ser Ile Asp Tyr	Val	Glu Asn Lys Leu	Tyr	Trp Ile Ser
1775		1780		1785	
Ser Gly	Asn Gly Thr Ile	Asn	Arg Cys Asn Leu	Asp	Gly Gly Asn
1790		1795		1800	
Leu Glu	Val Ile Glu Ser	Met	Lys Glu Glu Leu	Thr	Lys Ala Thr
1805		1810		1815	

Ala Leu Thr Ile Met Asp Lys	Lys Leu Trp Trp Ala Asp Gln Asn
1820	1825 1830
Leu Ala Gln Leu Gly Thr Cys	Ser Lys Arg Asp Gly Arg Asn Pro
1835	1840 1845
Thr Ile Leu Arg Asn Lys Thr	Ser Gly Val Val His Met Lys Val
1850	1855 1860
Tyr Asp Lys Glu Ala Gln Gln	Gly Ser Asn Ser Cys Gln Leu Asn
1865	1870 1875
Asn Gly Gly Cys Ser Gln Leu	Cys Leu Pro Thr Ser Glu Thr Thr
1880	1885 1890
Arg Thr Cys Met Cys Thr Val	Gly Tyr Tyr Leu Gln Lys Asn Arg
1895	1900 1905
Met Ser Cys Gln Gly Ile Glu	Ser Phe Leu Met Tyr Ser Val His
1910	1915 1920
Glu Gly Ile Arg Gly Ile Pro	Leu Glu Pro Ser Asp Lys Met Asp
1925	1930 1935
Ala Leu Met Pro Ile Ser Gly	Thr Ser Phe Ala Val Gly Ile Asp
1940	1945 1950
Phe His Ala Glu Asn Asp Thr	Ile Tyr Trp Thr Asp Met Gly Phe
1955	1960 1965
Asn Lys Ile Ser Arg Ala Lys	Arg Asp Gln Thr Trp Lys Glu Asp
1970	1975 1980
Ile Ile Thr Asn Gly Leu Gly	Arg Val Glu Gly Ile Ala Val Asp
1985	1990 1995
Trp Ile Ala Gly Asn Ile Tyr	Trp Thr Asp His Gly Phe Asn Leu
2000	2005 2010
Ile Glu Val Ala Arg Leu Asn	Gly Ser Phe Arg Tyr Val Ile Ile
2015	2020 2025
Ser Gln Gly Leu Asp Gln Pro	Arg Ser Ile Ala Val His Pro Glu
2030	2035 2040
Lys Gly Leu Leu Phe Trp Thr	Glu Trp Gly Gln Met Pro Cys Ile
2045	2050 2055

Gly Lys	Ala Arg	Leu Asp	Gly Ser	Glu Lys	Val Val	Leu Val	Ser
2060			2065			2070	
Met Gly	Ile Ala	Trp Pro	Asn Gly	Ile Ser	Ile Asp	Tyr Glu	Glu
2075			2080		2085		
Asn Lys	Leu Tyr	Trp Cys	Asp Ala	Arg Thr	Asp Lys	Ile Glu	Arg
2090			2095		2100		
Ile Asp	Leu Glu	Thr Gly	Gly Asn	Arg Glu	Met Val	Leu Ser	Gly
2105			2110		2115		
Ser Asn	Val Asp	Met Phe	Ser Val	Ala Val	Phe Gly	Ala Tyr	Ile
2120			2125		2130		
Tyr Trp	Ser Asp	Arg Ala	His Ala	Asn Gly	Ser Val	Arg Arg	Gly
2135			2140		2145		
His Lys	Asn Asp	Ala Thr	Glu Thr	Ile Thr	Met Arg	Thr Gly	Leu
2150			2155		2160		
Gly Val	Asn Leu	Lys Glu	Val Lys	Ile Phe	Asn Arg	Val Arg	Glu
2165			2170		2175		
Lys Gly	Thr Asn	Val Cys	Ala Arg	Asp Asn	Gly Gly	Cys Lys	Gln
2180			2185		2190		
Leu Cys	Leu Tyr	Arg Gly	Asn Ser	Arg Arg	Thr Cys	Ala Cys	Ala
2195			2200		2205		
His Gly	Tyr Leu	Ala Glu	Asp Gly	Val Thr	Cys Leu	Arg His	Glu
2210			2215		2220		
Gly Tyr	Leu Leu	Tyr Ser	Gly Arg	Thr Ile	Leu Lys	Ser Ile	His
2225			2230		2235		
Leu Ser	Asp Glu	Thr Asn	Leu Asn	Ser Pro	Ile Arg	Pro Tyr	Glu
2240			2245		2250		
Asn Pro	Arg Tyr	Phe Lys	Asn Val	Ile Ala	Leu Ala	Phe Asp	Tyr
2255			2260		2265		
Asn Gln	Arg Arg	Lys Gly	Thr Asn	Arg Ile	Phe Tyr	Ser Asp	Ala
2270			2275		2280		
His Phe	Gly Asn	Ile Gln	Leu Ile	Lys Asp	Asn Trp	Glu Asp	Arg
2285			2290		2295		

Gln Val	Ile Val	Glu Asn	Val	Gly Ser	Val Glu	Gly	Leu Ala	Tyr
2300			2305			2310		
His Arg	Ala Trp	Asp Thr	Leu	Tyr Trp	Thr Ser	Ser	Thr Thr	Ser
2315			2320			2325		
Ser Ile	Thr Arg	His Thr	Val	Asp Gln	Thr Arg	Pro	Gly Ala	Phe
2330			2335			2340		
Asp Arg	Glu Ala	Val Ile	Thr	Met Ser	Glu Asp	Asp	His Pro	His
2345			2350			2355		
Val Leu	Ala Leu	Asp Glu	Cys	Gln Asn	Leu Met	Phe	Trp Thr	Asn
2360			2365			2370		
Trp Asn	Glu Gln	His Pro	Ser	Ile Met	Arg Ser	Thr	Leu Thr	Gly
2375			2380			2385		
Lys Asn	Ala Gln	Val Val	Val	Ser Thr	Asp Ile	Leu	Thr Pro	Asn
2390			2395			2400		
Gly Leu	Thr Ile	Asp Tyr	Arg	Ala Glu	Lys Leu	Tyr	Phe Ser	Asp
2405			2410			2415		
Gly Ser	Leu Gly	Lys Ile	Glu	Arg Cys	Glu Tyr	Asp	Gly Ser	Gln
2420			2425			2430		
Arg His	Val Ile	Val Lys	Ser	Gly Pro	Gly Thr	Phe	Leu Ser	Leu
2435			2440			2445		
Ala Val	Tyr Asp	Asn Tyr	Ile	Phe Trp	Ser Asp	Trp	Gly Arg	Arg
2450			2455			2460		
Ala Ile	Leu Arg	Ser Asn	Lys	Tyr Thr	Gly Gly	Asp	Thr Lys	Ile
2465			2470			2475		
Leu Arg	Ser Asp	Ile Pro	His	Gln Pro	Met Gly	Ile	Ile Ala	Val
2480			2485			2490		
Ala Asn	Asp Thr	Asn Ser	Cys	Glu Leu	Ser Pro	Cys	Ala Leu	Leu
2495			2500			2505		
Asn Gly	Gly Cys	His Asp	Leu	Cys Leu	Leu Thr	Pro	Asn Gly	Arg
2510			2515			2520		
Val Asn	Cys Ser	Cys Arg	Gly	Asp Arg	Ile Leu	Leu	Glu Asp	Asn
2525			2530			2535		

Arg Cys	Val Thr Lys Asn Ser	Ser Cys Asn Ala Tyr	Ser Glu Phe
2540	2545	2550	
Glu Cys	Gly Asn Gly Glu Cys	Ile Asp Tyr Gln Leu	Thr Cys Asp
2555	2560	2565	
Gly Ile	Pro His Cys Lys Asp	Lys Ser Asp Glu Lys	Leu Leu Tyr
2570	2575	2580	
Cys Glu	Asn Arg Ser Cys Arg	Arg Gly Phe Lys Pro	Cys Tyr Asn
2585	2590	2595	
Arg Arg	Cys Ile Pro His Gly	Lys Leu Cys Asp Gly	Glu Asn Asp
2600	2605	2610	
Cys Gly	Asp Asn Ser Asp Glu	Leu Asp Cys Lys Val	Ser Thr Cys
2615	2620	2625	
Ala Thr	Val Glu Phe Arg Cys	Ala Asp Gly Thr Cys	Ile Pro Arg
2630	2635	2640	
Ser Ala	Arg Cys Asn Gln Asn	Ile Asp Cys Ala Asp	Ala Ser Asp
2645	2650	2655	
Glu Lys	Asn Cys Asn Asn Thr	Asp Cys Thr His Phe	Tyr Lys Leu
2660	2665	2670	
Gly Val	Lys Thr Thr Gly Phe	Ile Arg Cys Asn Ser	Thr Ser Leu
2675	2680	2685	
Cys Val	Leu Pro Thr Trp Ile	Cys Asp Gly Ser Asn	Asp Cys Gly
2690	2695	2700	
Asp Tyr	Ser Asp Glu Leu Lys	Cys Pro Val Gln Asn	Lys His Lys
2705	2710	2715	
Cys Glu	Glu Asn Tyr Phe Ser	Cys Pro Ser Gly Arg	Cys Ile Leu
2720	2725	2730	
Asn Thr	Trp Ile Cys Asp Gly	Gln Lys Asp Cys Glu	Asp Gly Arg
2735	2740	2745	
Asp Glu	Phe His Cys Asp Ser	Ser Cys Ser Trp Asn	Gln Phe Ala
2750	2755	2760	
Cys Ser	Ala Gln Lys Cys Ile	Ser Lys His Trp Ile	Cys Asp Gly
2765	2770	2775	

Glu Asp	Asp Cys Gly Asp	Gly	Leu Asp Glu Ser Asp	Ser Ile Cys
2780		2785		2790
Gly Ala	Ile Thr Cys Ala	Ala	Asp Met Phe Ser Cys	Gln Gly Ser
2795		2800		2805
Arg Ala	Cys Val Pro Arg	His	Trp Leu Cys Asp	Gly Glu Arg Asp
2810		2815		2820
Cys Pro	Asp Gly Ser Asp	Glu	Leu Ser Thr Ala	Gly Cys Ala Pro
2825		2830		2835
Asn Asn	Thr Cys Asp Glu	Asn	Ala Phe Met Cys	His Asn Lys Val
2840		2845		2850
Cys Ile	Pro Lys Gln Phe	Val	Cys Asp His Asp	Asp Asp Cys Gly
2855		2860		2865
Asp Gly	Ser Asp Glu Ser	Pro	Gln Cys Gly Tyr Arg	Gln Cys Gly
2870		2875		2880
Thr Glu	Glu Phe Ser Cys	Ala	Asp Gly Arg Cys	Leu Leu Asn Thr
2885		2890		2895
Gln Trp	Gln Cys Asp Gly	Asp	Phe Asp Cys Pro	Asp His Ser Asp
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Glu Ala	Pro Leu Asn Pro	Lys	Cys Lys Ser Ala	Glu Gln Ser Cys
2915		2920		2925
Asn Ser	Ser Phe Phe Met	Cys	Lys Asn Gly Arg	Cys Ile Pro Ser
2930		2935		2940
Gly Gly	Leu Cys Asp Asn	Lys	Asp Asp Cys Gly	Asp Gly Ser Asp
2945		2950		2955
Glu Arg	Asn Cys His Ile	Asn	Glu Cys Leu Ser	Lys Lys Val Ser
2960		2965		2970
Gly Cys	Ser Gln Asp Cys	Gln	Asp Leu Pro Val	Ser Tyr Lys Cys
2975		2980		2985
Lys Cys	Trp Pro Gly Phe	Gln	Leu Lys Asp Asp	Gly Lys Thr Cys
2990		2995		3000
Val Asp	Ile Asp Glu Cys	Ser	Ser Gly Phe Pro	Cys Ser Gln Gln
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Cys Ile	Asn Thr Tyr Gly	Thr	Tyr Lys Cys Leu	Cys	Thr Asp Gly
3020		3025		3030	
Tyr Glu	Ile Gln Pro Asp	Asn	Pro Asn Gly Cys	Lys	Ser Leu Ser
3035		3040		3045	
Asp Glu	Glu Pro Phe Leu	Ile	Leu Ala Asp His	His	Glu Ile Arg
3050		3055		3060	
Lys Ile	Ser Thr Asp Gly	Ser	Asn Tyr Thr Leu	Leu	Lys Gln Gly
3065		3070		3075	
Leu Asn	Asn Val Ile Ala	Ile	Asp Phe Asp Tyr	Arg	Glu Glu Phe
3080		3085		3090	
Ile Tyr	Trp Ile Asp Ser	Ser	Arg Pro Asn Gly	Ser	Arg Ile Asn
3095		3100		3105	
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Ala Val	Pro Asn Ala Leu	Ala	Val Asp Trp Ile	Gly	Lys Asn Leu
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Tyr Trp	Ser Asp Thr Glu	Lys	Arg Ile Ile Glu	Val	Ser Lys Leu
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Asn Gly	Leu Tyr Pro Thr	Ile	Leu Val Ser Lys	Arg	Leu Lys Phe
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Pro Arg	Asp Leu Ser Leu	Asp	Pro Gln Ala Gly	Tyr	Leu Tyr Trp
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Ile Asp	Cys Cys Glu Tyr	Pro	His Ile Gly Arg	Val	Gly Met Asp
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Gly Thr	Asn Gln Ser Val	Val	Ile Glu Thr Lys	Ile	Ser Arg Pro
3200		3205		3210	
Met Ala	Leu Thr Ile Asp	Tyr	Val Asn Arg Arg	Leu	Tyr Trp Ala
3215		3220		3225	
Asp Glu	Asn His Ile Glu	Phe	Ser Asn Met Asp	Gly	Ser His Arg
3230		3235		3240	
His Lys	Val Pro Asn Gln	Asp	Ile Pro Gly Val	Ile	Ala Leu Thr
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Leu Phe	Glu Asp Tyr Ile	Tyr	Trp Thr Asp Gly	Lys	Thr Lys Ser
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Leu Ser	Arg Ala His Lys	Thr	Ser Gly Ala Asp	Arg	Leu Ser Leu
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Ile Tyr	Ser Trp His Ala	Ile	Thr Asp Ile Gln	Val	Tyr His Ser
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Tyr Arg	Gln Pro Asp Val	Ser	Lys His Leu Cys	Met	Ile Asn Asn
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Thr Cys	Ala Cys Pro Thr	Asn	Phe Tyr Leu Ala	Ala	Asp Asn Arg
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Thr Cys	Leu Ser Asn Cys	Thr	Ala Ser Gln Phe	Arg	Cys Lys Thr
3350		3355		3360	
Asp Lys	Cys Ile Pro Phe	Trp	Trp Lys Cys Asp	Thr	Val Asp Asp
3365		3370		3375	
Cys Gly	Asp Gly Ser Asp	Glu	Pro Asp Asp Cys	Pro	Glu Phe Arg
3380		3385		3390	
Cys Gln	Pro Gly Arg Phe	Gln	Cys Gly Thr Gly	Leu	Cys Ala Leu
3395		3400		3405	
Pro Ala	Phe Ile Cys Asp	Gly	Glu Asn Asp Cys	Gly	Asp Asn Ser
3410		3415		3420	
Asp Glu	Leu Asn Cys Asp	Thr	His Val Cys Leu	Ser	Gly Gln Phe
3425		3430		3435	
Lys Cys	Thr Lys Asn Gln	Lys	Cys Ile Pro Val	Asn	Leu Arg Cys
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Asn Gly	Gln Asp Asp Cys	Gly	Asp Glu Glu Asp	Glu	Arg Asp Cys
3455		3460		3465	
Pro Glu	Asn Ser Cys Ser	Pro	Asp Tyr Phe Gln	Cys	Lys Thr Thr
3470		3475		3480	
Lys His	Cys Ile Ser Lys	Leu	Trp Val Cys Asp	Glu	Asp Pro Asp
3485		3490		3495	

Cys Ala	Asp Ala Ser Asp	Glu Ala Asn Cys Asp	Lys Lys Thr Cys
3500		3505	3510
Gly Pro	His Glu Phe Gln Cys	Lys Asn Asn Asn Cys	Ile Pro Asp
3515		3520	3525
His Trp	Arg Cys Asp Ser	Gln Asn Asp Cys Ser	Asp Asn Ser Asp
3530		3535	3540
Glu Glu	Asn Cys Lys Pro	Gln Thr Cys Thr Leu	Lys Asp Phe Leu
3545		3550	3555
Cys Ala	Asn Gly Asp Cys	Val Ser Ser Arg Phe	Trp Cys Asp Gly
3560		3565	3570
Asp Phe	Asp Cys Ala Asp	Gly Ser Asp Glu Arg	Asn Cys Glu Thr
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Ser Cys	Ser Lys Asp Gln Phe	Arg Cys Ser Asn Gly	Gln Cys Ile
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Pro Ala	Lys Trp Lys Cys	Asp Gly His Glu Asp	Cys Lys Tyr Gly
3605		3610	3615
Glu Asp	Glu Lys Ser Cys	Glu Pro Ala Ser Pro	Thr Cys Ser Ser
3620		3625	3630
Arg Glu	Tyr Ile Cys Ala	Ser Asp Gly Cys Ile	Ser Ala Ser Leu
3635		3640	3645
Lys Cys	Asn Gly Glu Tyr	Asp Cys Ala Asp Gly	Ser Asp Glu Met
3650		3655	3660
Asp Cys	Val Thr Glu Cys	Lys Glu Asp Gln Phe	Arg Cys Lys Asn
3665		3670	3675
Lys Ala	His Cys Ile Pro	Ile Arg Trp Leu Cys	Asp Gly Ile His
3680		3685	3690
Asp Cys	Val Asp Gly Ser	Asp Glu Glu Asn Cys	Glu Arg Gly Gly
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Lys Leu	His Phe Trp Val	Cys Asp Gly Glu Asp	Asp Cys Gly Asp
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Asn Ser	Asp Glu Ala Pro	Asp	Met Cys Val Lys Phe	Leu Cys Pro
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Ser Thr	Arg Pro His Arg	Cys	Arg Asn Asn Arg	Ile Cys Leu Gln
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Ser Glu	Gln Met Cys Asn	Gly	Ile Asp Glu Cys Gly	Asp Asn Ser
3770		3775		3780
Asp Glu	Asp His Cys Gly	Gly	Lys Leu Thr Tyr Lys	Ala Arg Pro
3785		3790		3795
Cys Lys	Lys Asp Glu Phe	Ala	Cys Ser Asn Lys Lys	Cys Ile Pro
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Met Asp	Leu Gln Cys Asp	Arg	Leu Asp Asp Cys Gly	Asp Gly Ser
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Asp Glu	Gln Gly Cys Arg	Ile	Ala Pro Thr Glu Tyr	Thr Cys Glu
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Asp Asn	Val Asn Pro Cys	Gly	Asp Asp Ala Tyr Cys	Asn Gln Ile
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Lys Thr	Ser Val Phe Cys	Arg	Cys Lys Pro Gly Phe	Gln Arg Asn
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Met Lys	Asn Arg Gln Cys	Glu	Asp Leu Asn Glu Cys	Leu Val Phe
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Gly Thr	Cys Ser His Gln	Cys	Ile Asn Val Glu Gly	Ser Tyr Lys
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Gln Gln	Ile Ser His Ile	Glu	His Asn Ser Arg Ile	Thr Gly Met
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Asp Val	Tyr Tyr Gln Arg	Asp	Met Ile Ile Trp Ser	Thr Gln Phe
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Asn Pro	Gly Gly Ile Phe	Tyr	Lys Arg Ile His	Gly	Arg Glu Lys
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Asn Cys	Thr Arg Leu Leu	Thr	Asn Met Ala Gly	Glu	Pro Tyr Ala
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Ile Ala	Val Asn Pro Lys	Arg	Gly Met Met Tyr	Trp	Thr Val Val
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Gly Asp	His Ser His Ile	Glu	Glu Ala Ala Met	Asp	Gly Thr Leu
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Arg Arg	Ile Leu Val Gln	Lys	Asn Leu Gln Arg	Pro	Thr Gly Leu
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Ala Val	Asp Tyr Phe Ser	Glu	Arg Ile Tyr Trp	Ala	Asp Phe Glu
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Leu Ser	Ile Ile Gly Ser	Val	Leu Tyr Asp Gly	Ser	Asn Ser Val
4130		4135		4140	
Val Ser	Val Ser Ser Lys	Gln	Gly Leu Leu His	Pro	His Arg Ile
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Ala Leu	Asn Ile Asp Lys	Thr	Lys Gly Val Leu	Ile	Ser His Arg
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Tyr Lys	Gln Leu Asp Leu	Pro	Asn Pro Cys Leu	Asp	Leu Ala Cys
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Asp	Ile	Phe	Cys	Asn	Cys	Thr	Asn	Gly	Lys	Ile	Ala	Ser	Ser	Cys
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Gln	Leu	Cys	Asp	Gly	Tyr	Cys	Tyr	Asn	Gly	Gly	Thr	Cys	Gln	Leu
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Ser Gly Thr Gln Cys Glu Arg Pro Ala Pro Lys Ser Ser Lys Ser
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Asp His Ile Ser Thr Arg Ser Ile Ala Ile Ile Val Pro Leu Val
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Leu Leu Val Thr Leu Ile Thr Thr Leu Val Ile Gly Leu Val Leu
4490 4495 4500

Cys Lys Arg Lys Arg Arg Thr Lys Thr Ile Arg Arg Gln Pro Ile
4505 4510 4515

Ile Asn Gly Gly Ile Asn Val Glu Ile Gly Asn Pro Ser Tyr Asn
4520 4525 4530

Met Tyr Glu Val Asp His Asp His Asn Asp Gly Gly Leu Leu Asp
4535 4540 4545

Pro Gly Phe Met Ile Asp Pro Thr Lys Ala Arg Tyr Ile Gly Gly
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Gly Pro Ser Ala Phe Lys Leu Pro His Thr Ala Pro Pro Ile Tyr
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Leu Asn Ser Asp Leu Lys Gly Pro Leu Thr Ala Gly Pro Thr Asn
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Tyr Ser Asn Pro Val Tyr Ala Lys Leu Tyr Met Asp Gly Gln Asn
4595 4600 4605

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cgaccagtgg	ccctgacctt	gctgactttg	tgcttgggtg	tgctgatagg	gctggcgacc	300
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gtactgatta	catgattatc	tggagaaaat	aagatgtctt	tgaataacat	gttggtctca	1980
agaaaacagt	tttaacgttt	tcttaaaaat	aaatcttttg	aggtgagctt	atggcatcaa	2040

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<210> 35
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 35

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 Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
 35 40 45
 Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
 50 55 60
 Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
 65 70 75 80
 Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
 85 90 95
 Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
 100 105 110
 Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
 115 120 125
 Ala Gly Ala His Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His
 130 135 140
 Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp
 145 150 155 160
 Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn
 165 170 175
 Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe
 180 185 190
 Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala
 195 200 205
 Trp Leu Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile
 210 215 220
 Ile Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
 225 230 235 240
 Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val
 245 250 255

Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro
260 265

Pro Glu Thr Leu Gly Glu Gly Asp
275 280

<210> 36
<211> 2323
<212> DNA
<213> Homo sapiens

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<210> 37
<211> 307
<212> PRT
<213> Homo sapiens

<400> 37

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Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
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Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg
35 40 45
Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly
50 55 60
Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn
65 70 75 80
Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr
85 90 95
Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly
100 105 110
Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys
115 120 125

Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu
130 135 140

Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg
145 150 155 160

Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr
165 170 175

Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
180 185 190

Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu
195 200 205

Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp
210 215 220

Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp
225 230 235 240

Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr
245 250 255

Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe
260 265 270

Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala
275 280 285

Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly
290 295 300

Glu Gly Asp
305

<210> 38

<211> 2714

<212> DNA

<213> Homo sapiens

<400> 38

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<210> 39
<211> 769
<212> PRT
<213> Homo sapiens

<400> 39

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Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
35 40 45
Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
50 55 60
Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65 70 75 80
Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
85 90 95
Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
100 105 110
Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
115 120 125
Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
130 135 140
Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145 150 155 160
Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
165 170 175
Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
180 185 190
Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
195 200 205
Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
210 215 220
Val Asn Ala Ala Phe Tyr Arg Lys Leu Arg Lys Arg Ala Ala Lys Val
225 230 235 240
Ser Ala Arg His Pro Lys Pro Leu Gly Arg Leu Leu Ala Gln Arg Gln
245 250 255
Gln His Ser Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala

270

His	Leu	Ser	Leu	Cys	Ser	Leu	Glu	Phe	Tyr	Arg	Ala	Asn	Asp	Thr	Ala
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Arg	Cys	Pro	Gly	Gly	Gly	Pro	Ala	Val	Val	Ser	Cys	Val	Pro	Gly	Pro
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Val	Tyr	Ala	Ala	Ser	Ser	Gly	Gln	Lys	Lys	Gln	Gln	Gln	Ser	Lys	Pro
	305				310					315					320
Gln	Gly	Glu	Ala	Arg	Val	Arg	Leu	Lys	Gly	Gly	Ala	His	Pro	Gly	Glu
				325					330					335	
Gly	Arg	Val	Glu	Val	Leu	Lys	Ala	Ser	Thr	Trp	Gly	Thr	Val	Cys	Asp
			340					345					350		
Arg	Lys	Trp	Asp	Leu	His	Ala	Ala	Ser	Val	Val	Cys	Arg	Glu	Leu	Gly
		355					360					365			
Phe	Gly	Ser	Ala	Arg	Glu	Ala	Leu	Ser	Gly	Ala	Arg	Met	Gly	Gln	Gly
	370					375					380				
Met	Gly	Ala	Ile	His	Leu	Ser	Glu	Val	Arg	Cys	Ser	Gly	Gln	Glu	Leu
	385				390					395					400
Ser	Leu	Trp	Lys	Cys	Pro	His	Lys	Asn	Ile	Thr	Ala	Glu	Asp	Cys	Ser
				405					410					415	
His	Ser	Gln	Asp	Ala	Gly	Val	Arg	Cys	Asn	Leu	Pro	Tyr	Thr	Gly	Ala
			420					425					430		
Glu	Thr	Arg	Ile	Arg	Leu	Ser	Gly	Arg	Ser	Gln	His	Glu	Gly	Arg	
	435						440					445			
Val	Glu	Val	Gln	Ile	Gly	Gly	Pro	Gly	Pro	Leu	Arg	Trp	Gly	Leu	Ile
	450					455					460				
Cys	Gly	Asp	Asp	Trp	Gly	Thr	Leu	Glu	Ala	Met	Val	Ala	Cys	Arg	Gln
	465				470					475					480
Leu	Gly	Leu	Gly	Tyr	Ala	Asn	His	Gly	Leu	Gln	Glu	Thr	Trp	Tyr	Trp
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			500					505					510		
Gly	Thr	Glu	Leu	Ser	Leu	Asp	Gln	Cys	Ala	His	His	Gly	Thr	His	Ile
	515						520					525			
Thr	Cys	Lys	Arg	Thr	Gly	Thr	Arg	Phe	Thr	Ala	Gly	Val	Ile	Cys	Ser
	530					535					540				
Glu	Thr	Ala	Ser	Asp	Leu	Leu	His	Ser		Ala	Leu	Val	Gln	Glu	Thr
	545				550					555					560
Ala	Tyr	Ile	Glu	Asp	Arg	Pro	Leu	His	Met	Leu	Tyr	Cys	Ala	Ala	Glu
				565					570					575	
Glu	Asn	Cys	Leu	Ala	Ser	Ser	Ala	Arg	Ser	Ala	Asn	Trp	Pro	Tyr	Gly
			580					585					590		
His	Arg	Arg	Leu	Leu	Arg	Phe	Ser	Ser	Gln	Ile	His	Asn	Leu	Gly	Arg

595	600	605
Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu 610 615 620		
Cys His Gly His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile 625 630 635 640		
Leu Thr Pro Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe 645 650 655		
Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu 660 665 670		
Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu 675 680 685		
Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys 690 695 700		
Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val 705 710 715 720		
Ala Glu Ser Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr 725 730 735		
Asp Gly His Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe 740 745 750		
Ser Glu Glu Ala His Arg Arg Phe Glu Arg Ser Pro Gly Gln Thr Ser 755 760 765		

Thr

<210> 40
 <211> 1877
 <212> DNA
 <213> Homo sapiens

<400> 40
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 accacgaggt cccgaggggg gacactcgac ggacacgagt gacgggaaat gtgcatctac 1740
 actagcgcgc gacagctaga gcgatgacgg cagggacgtc tcgcagccta ccagcaacgc 1800
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 cagcatgaac tcccagg 1877

<210> 41
 <211> 400
 <212> PRT
 <213> Homo sapiens

<400> 41

Met Asn Lys Lys Lys Pro Leu His Ser Lys Ser Ser Arg Ile His Gln
 1 5 10 15

Gln Ile Ile Val Gln Leu Asp Ser Leu Pro Pro Pro Val Phe Ser Glu
 20 25 30

Gln Val Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu
 35 40 45

Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr
 50 55 60

Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln

65	70					75					80				
Gln Lys Met Ala Arg	Glu Pro Ala Thr	Leu Lys Asp Ser	Leu Glu Gln												
85		90		95											
Asp Leu Asn Asn Met	Asn Lys Phe	Leu Glu Lys Leu Arg	Pro Leu Ser												
100		105		110											
Gly Ser Glu Ala Pro	Arg Leu Pro	Gln Asp Pro Val	Gly Met Arg Arg												
115		120		125											
Gln Leu Gln Glu Glu	Leu Glu Glu Val	Lys Ala Arg	Leu Gln Pro Tyr												
130		135		140											
Met Ala Glu Ala His	Glu Leu Val Gly	Trp Asn Leu Glu Gly	Leu Arg												
145		150		155											
Gln Gln Leu Lys Pro	Tyr Thr Met Asp	Leu Met Glu Gln Val	Ala Leu												
165		170		175											
Arg Val Gln Glu Leu	Gln Glu Gln Leu	Arg Val Val Gly	Glu Asp Thr												
180		185		190											
Lys Ala Gln Leu Leu	Gly Gly Val Asp	Glu Ala Trp Ala	Leu Leu Gln												
195		200		205											
Gly Leu Gln Ser Arg	Val Val His His	Thr Gly Arg Phe	Lys Glu Leu												
210		215		220											
Phe His Pro Tyr Ala	Glu Ser Leu Val	Ser Gly Ile Gly	Arg His Val												
225		230		235											
Gln Glu Leu His Arg	Ser Val Ala Pro	His Ala Pro Ala	Ser Pro Ala												
245		250		255											
Arg Leu Ser Arg Cys	Val Gln Val Leu	Ser Arg Lys Leu	Thr Leu Lys												
260		265		270											
Ala Lys Ala Leu His	Ala Arg Ile	Gln Gln Asn Leu	Asp Gln Leu Arg												
275		280		285											
Glu Glu Leu Ser Arg	Ala Phe Ala Gly	Thr Gly Thr	Glu Glu Gly Ala												
290		295		300											
Gly Pro Asp Pro Gln	Met Leu Ser Glu	Glu Val Arg Gln	Arg Leu Gln												
305		310		315											
Ala Phe Arg Gln Asp	Thr Tyr Leu Gln	Ile Ala Ala Phe	Thr Arg Ala												
325		330		335											
Ile Asp Gln Glu Thr	Glu Glu Val Gln	Gln Gln Leu Ala	Pro Pro Pro												
340		345		350											
Pro Gly His Ser Ala	Phe Ala Pro	Glu Phe Gln Gln	Thr Asp Ser Gly												
355		360		365											
Lys Val Leu Ser Lys	Leu Gln Ala Arg	Leu Asp Asp	Leu Trp Glu Asp												
370		375		380											
Ile Thr His Ser Leu	His Asp Gln Gly	His Ser His	Leu Gly Asp Pro												
385		390		395											
400															

<211> 2128
<212> DNA
<213> Homo sapiens

<400> 42
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acaagcgctg ggggtgcagca aaaccatcca ggctgggacag tggctggaca gttccaagaa 180
aagaaacgct tcaactgaaga agtcattgaa tacttccaga agaaagttag ccagtgcat 240
ctgaaaaatcc tgctgactag cgatgaagcc tggaagagat ttgtgcgtgt ggctgaattg 300
cccaggggaag aggcagatgc tctctatgaa gctctgaaga atcttacacc atatgtgact 360
attgaggaca aagacatgca gcaaaaagaa cagcagttta gggagtgggt ttgaaagag 420
tttctctaaa lcagatggaa gattcaggag tccatagaaa ggctctgtgt cattgcaaat 480
gagattgaaa aggtccacag aggctgcgtc atcgccaatg tgggtgtctgg ctccactggc 540
atcctgtctg tcaattggcgt tatgttgcca ccatttacag cagggtctgag cctgagcatt 600
actgcagctg gggtagggct ggaatagca tctgccacgg ctgggactgc ctccagcatt 660
gtggagaaca catacacaag gtcagcagaa ctcacagcca gcaggctgac tgcaaccagc 720
actgaccaat tggaggcatt aagggaacatt ctgcatgaca tcacacccaa tgtgctttcc 780
tttgacttg attttgacga agccacaaaa atgattgcga atgatgtcca taaactcagg 840
agatctaaag ccactgttgg acgccccttg attgcttggc gatatgtacc tataaatgtt 900
gttgagacac tgagaacacg tggggccccc acccgatag tgagaaaagt agcccggaac 960
ctgggcaagg ccacttcagg tgtccttgtt gtgctggatg tagtcaacct tgtgcaagac 1020
tcactggact tgcacaaggg ggcaaaatcc gagtctgctg agtcgctgag gcagtgggct 1080
caggagctgg agggagaatc caatgagctc acccatatcc atcagagtct aaaagcaggc 1140
tagggccaat tgtgtcggga agtcaggagc ccaaacgga gggactggct gaagccatgg 1200
cagaagaacg tggattgtga agatttcatt gacatttatt agtccccaa attaataact 1260
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ggacacttat cacttcccc atcaataccc ttgtgatttc ttatgcctgt ctttacttta 1380
atctccta at cctgtcagct gaggaggatg tatgtcacct caggaccatg tgataattgc 1440
gttaactgca caaattgtag agcatgtgtg ttggaacaat atgaaatctg ggcaccttga 1500
aaaaagaaca ggataacagc aattgttcag ggaataagag agataacctt aaactctgac 1560
caacagttag ccgggtggaa cagagtcata tttctcttct tcaaaaagca aatgggagaa 1620
atatcgctga attctttttc tcagcaagga acatccctga gaaagagaat gcacccctga 1680
gggtgggtct ataaatggcc tccttgggtg tggccatctt ctatggtcga gactgtaggg 1740

atgaaataaaa cccagctctc ccatagtgtc cccagggtta ttaggaagag gaaattcccc 1800
 cctaataaat tttggctcaga cgggttgctc tcaaaaccct gtctcctgat aagatgttat 1860
 caatgacaat ggtgcctgaa acctcattag caattttaat ttctccccg tctgtggtc 1920
 ctgtgatctc accctgctc cacttgctt gtgatattct attacctgt gaagtaggtg 1980
 atctttgtga cccacaccct attcattacac tccctccctc ttgaaagtc cctaataaaa 2040
 acttgctggt ttgagcgtt gtgaggcatc acggaacctc ctgagtgtg atgtctcccc 2100
 tggacacctc gcttataaat ttcaaaaa 2128

<210> 43
 <211> 348
 <212> PRT
 <213> Homo sapiens

<400> 43

Met Gly Ser Trp Val Gln Leu Ile Thr Ser Val Gly Val Gln Gln Asn
 1 5 10 15
 His Pro Gly Trp Thr Val Ala Gly Gln Phe Gln Glu Lys Lys Arg Phe
 20 25 30
 Thr Glu Glu Val Ile Glu Tyr Phe Gln Lys Lys Val Ser Pro Val His
 35 40 45
 Leu Lys Ile Leu Leu Thr Ser Asp Glu Ala Trp Lys Arg Phe Val Arg
 50 55 60
 Val Ala Glu Leu Pro Arg Glu Glu Ala Asp Ala Leu Tyr Glu Ala Leu
 65 70 75 80
 Lys Asn Leu Thr Pro Tyr Val Thr Ile Glu Asp Lys Asp Met Gln Gln
 85 90 95
 Lys Glu Gln Gln Phe Arg Glu Trp Phe Leu Lys Glu Phe Pro Gln Ile
 100 105 110
 Arg Trp Lys Ile Gln Glu Ser Ile Glu Arg Leu Arg Val Ile Ala Asn
 115 120 125
 Glu Ile Glu Lys Val His Arg Gly Cys Val Ile Ala Asn Val Val Ser
 130 135 140
 Gly Ser Thr Gly Ile Leu Ser Val Ile Gly Val Met Leu Ala Pro Phe
 145 150 155 160
 Thr Ala Gly Leu Ser Leu Ser Ile Thr Ala Ala Gly Val Gly Leu Gly
 165 170 175
 Ile Ala Ser Ala Thr Ala Gly Ile Ala Ser Ser Ile Val Glu Asn Thr
 180 185 190
 Tyr Thr Arg Ser Ala Glu Leu Thr Ala Ser Arg Leu Thr Ala Thr Ser
 195 200 205
 Thr Asp Gln Leu Glu Ala Leu Arg Asp Ile Leu His Asp Ile Thr Pro
 210 215 220

Asn Val Leu Ser Phe Ala Leu Asp Phe Asp Glu Ala Thr Lys Met Ile
 225 230 235 240

Ala Asn Asp Val His Thr Leu Arg Arg Ser Lys Ala Thr Val Gly Arg
 245 250 255

Pro Leu Ile Ala Trp Arg Tyr Val Pro Ile Asn Val Val Glu Thr Leu
 260 265 270

Arg Thr Arg Gly Ala Pro Thr Arg Ile Val Arg Lys Val Ala Arg Asn
 275 280 285

Leu Gly Lys Ala Thr Ser Gly Val Leu Val Val Leu Asp Val Val Asn
 290 295 300

Leu Val Gln Asp Ser Leu Asp Leu His Lys Gly Ala Lys Ser Glu Ser
 305 310 315 320

Ala Glu Ser Leu Arg Gln Trp Ala Gln Glu Leu Glu Glu Asn Leu Asn
 325 330 335

Glu Leu Thr His Ile His Gln Ser Leu Lys Ala Gly
 340 345

<210> 44
 <211> 988
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> n = a or c or g or t

<220>
 <221> CDS
 <222> (129)..(971)

<400> 44
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agctcacagt agcccgccgg cccagggcaa tccgaccaca ttctactctc accgtgtgag 120

gaatccag atg cag gcc aag tac agc agc agc agg gac atg ctg gat gat 170
 Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp
 1 5 10

gat ggg gac acc acc atg agc ctg cat tct caa gcc tct gcc aca act 218
 Asp Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
 15 20 25 30

cgg cat cca gag ccc cgg cgc aca gtt ttt cag tac tac cag ctc tcc 266
 Arg His Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser
 35 40 45

aat act ggt caa gac acc att tct caa atg gaa gaa aga tta gga aat 314
 Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn
 50 55 60

acg tcc caa gag ttg caa tct ctt caa gtc cag aat ata aag ctt gca 362
 Thr Ser Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala
 65 70 75

gga agt ctg cag cat gtg gct gaa aaa ctc tgt cgt gag ctg tat aac	410
Gly Ser Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn	
80 85 90	
aaa gct gga ggc tat aca aga aac atg gtg cca gca tct gct tct tct	458
Lys Ala Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser	
95 100 105 110	
gag agc ctc agg cag ctt cca cac atg ggg gaa agt gca gca gca cac	506
Glu Ser Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His	
115 120 125	
agg tgc agc cct tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc	554
Arg Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys	
130 135 140	
tac cag ttc tat aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc	602
Tyr Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe	
145 150 155	
tgc ctt agt gaa aac tct acc atg ctg aag ata aac aaa caa gaa gac	650
Cys Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp	
160 165 170	
ctg gaa ttt gcc gcg tct cag agc tac tct gag ttt ttc tac tct tat	698
Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr	
175 180 185 190	
tgg aca ggg ctt ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg	746
Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met	
195 200 205	
gat gga acc cct ttc act tct gaa ctg ttc cat att ata ata gat gtc	794
Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val	
210 215 220	
acc agc cca aga agc aga gac tgt gtg gcc atc ctt aat ggg atg atc	842
Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile	
225 230 235	
ttc tca aag gac tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg	890
Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg	
240 245 250	
gca gga atg gtg aag cca gag agc ctc cat gtc ccc cct gaa aca tta	938
Ala Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu	
255 260 265 270	
ggc gaa ggt gac atg cat cat cat cat cat cat tagcctaggt tctagac	988
Gly Glu Gly Asp Met His His His His His His	
275 280	

<210> 45
 <211> 281
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> n = a or c or g or t

 <400> 45

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly
1 5 10 15

Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr Arg His
20 25 30

Pro Glu Pro Arg Arg Thr Val Phe Gln Tyr Tyr Gln Leu Ser Asn Thr
35 40 45

Gly Gln Asp Thr Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser
50 55 60

Gln Glu Leu Gln Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser
65 70 75 80

Leu Gln His Val Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala
85 90 95

Gly Gly Tyr Thr Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser
100 105 110

Leu Arg Gln Leu Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys
115 120 125

Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
130 135 140

Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu
145 150 155 160

Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu
165 170 175

Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr
180 185 190

Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly
195 200 205

Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr Ser
210 215 220

Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe Ser
225 230 235 240

Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala Gly
245 250 255

Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly Glu
260 265 270

Gly Asp Met His His His His His His
275 280